

STIC Search Report Biotech-Chem Library

STIC Database therefore it in the control of the co

TO: Jeanine Goldberg Location: rem/2D15/2C70

Art Unit: 1634

Wednesday, July 13, 2005

Case Serial Number: 10/681199

From: Toby Port

Location: Biotech-Chem Library

REM-1A59

Phone: 571-272-2523

toby.port@uspto.gov

Secreta Notes

Examiner Goldberg,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Toby Port X22523



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From: Sent:

Goldberg, Jeanine Tuesday, July 05, 2005 6:20 AM

To: Subject: STIC-Biotech/ChemLib 10/681199- Search

Please search SEQ ID NO: 1 in all databases. Please also do a mer search of SEQ ID NO: 1.

THANK YOU

Jeanine Anne Goldberg 1634 571-272-0743 **REM 2D15**

2010

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Searcher:_ Searcher Phone: 2-Date Searcher Picked up:_ Date Completed:_

Searcher Prep/Rev. Time:_ Online Time:_

Type of Search

NA#:	AA#:
Interference:	SPDI:
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Inventor:	Litigation:

Vendors and cost where applicable

STN: DIALOG: QUESTEL/ORBIT: LEXIS/NEXIS:

SEQUENCE SYSTEM:_ WWW/Internet:__

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July 8, 2005, 04:46:25; Search time 758 Seconds (without alignments) 9863.632 Million cell updates/sec US-10-681-199-1 1263 1 atgcctcttcaggttagcga......gaacagaactaaaatcttaa 1263 Title: Perfect score:

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4390206 seqs, 2959870667 residues Searched:

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8780412 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Adb16964 Human DYX	Adb16965 cDNA sequ	Adc30210 Human nov	Adb16939 Pygmy chi	Adm01890 Human cDN	Adb16933 Chimpanze	Adb16935 Gorilla D	Adb16937 Orangutan	Adc32116 Human nov	Ach35463 Human end	Ach23091 Human adu	Aas70018 DNA encod	Adb16927 Human DYX	Adb16928 Human DYX	Aac30498 Human sec	Aac26799 Human sec	Aaa45298 Human sec	Aaa45298 Human sec	Adb16924 cDNA segu	Adb16932 Reverse R
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                                                                            New isolated, purified DYXC1 nucleic acid for studying brain processes, eg. reading, phonological processing, rapid naming or verbal short-term memory, or for diagnosing dyslexia or assessing the predisposition to dyslexia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention relates to a novel isolated human gene DYXC1 that is functionally related to dyslexia, more particularly it describes single nucleotide polymorphisms thought to predispose an individual in to developing dyslexia. This is a neurological disorder with a genetic basis (DYXC1 has been isolated to chromosome 15q21), which manifests itself as a specific reading disability. Specifically, DYXC1 is can be useful in study of brain processes such as reading, phonological processing, rapid naming and verbal short-term memory. Accordingly, the present invention describes methods and materials for analysing allelic variations in the DYXC1 gene, and also provides DYXC1 as an antigen for the production of antibodies used in the diagnosis of dyslexia. This polynuclectide is the CDNA sequence of the wild type human DYXC1 mRNA of the invention.
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                                                                                                                                                                                                                                                                                                   New isolated, purified DYXC1 nucleic acid for studying brain processes, e.g. reading, phonological processing, rapid naming or verbal short-term memory, or for diagnosing dyslexia or assessing the predisposition to
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100.0%; Pred. No. 0;
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WO2003068814-A1
                                     21-AUG-2003
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The invention relates to 971 novel human cDNA sequences (ADC29919-ADC31889) and the polypeptides they encode (ADC30890-ADC31860). The invention also relates to nucleic acid sequences over 99% identical with the novel human cDNAs. The invention additionally encompasses expression vectors and host cells comprising a nucleic acid of the invention; the recombinant production of a polypeptide of the invention; an antibody against a polypeptide of the invention; and methods of detecting polymucleotides or polypeptides of the invention; and methods of identifying a compound which binds to a polypeptide of the invention. The invention further discloses methods of peventing, treating or andiorating a medical condition; kits comprising polymucleotide probes and/or monoclonal antibodies for carrying out the methods of the invention. The invention; methods for the identification of compounds that modulate the invention; methods for the identification of compounds that modulate the corpression or activity of the polymucleotide and/or polypeptides of the invention and 767 contig sequences corresponding to the cDNA sequences of the invention are useful in diagnostics, drug screening, forcemsics, gene mapping, in the identification of mutations responsible for genetic disorders or other types of and and products dependent on DNA and amino acid sequences. They are also used for treating diseases such as Parkinson's disease, Alzheimer's disorders, wounds, burns, ulcers, osteoporosis, anemia, platelet contigues, ulcers, osteoporosis, anemia, platelet contigues, ulcers, osteoporosis, and producted and not the recombinant production of a protein The polypeptides are also useful in generating antibodies, as molecular weight markers, and as food supplements. The present sequence represents a specifically and electronic form part of the printed specification, but was continued to the contract of the printed specification, but was sequenced.
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antiulcer; osteopathic; immunosuppressive; antiinflammatory; cytostatic; gene therapy; chromosome 15q21.3; gene; ss.
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Zhou P, Ghosh M, Wang D, Ma Y, Asundi V,
Haley-Vicente D, Drmanac RT;
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ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 292; 1185pp; English.
                                                                                                                                                                                                     24-SEP-2002; 2002WO-US030474.
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P-PSDB; ADC31181.
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                                                                       Homo sapiens
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                                                              npanzee, DYXC1; dyslexia; neurological disorder;
phonological processing; rapid naming;
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                               Pygmy chimpanzee DYXC1 cDNA sequence.
                                                                                                                                                                Location/Qualifiers
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99.6%;
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                                                                chimpanzee;
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                                                                                                 verbal short-term memory.
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disability;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a novel human polynuclectide and the encoded polypeptide. A polynuclectide of the invention may have a use in gene therapy. An oligonuclectide of the invention ADM06202-ADM06773 is useful as a primer for synthesizing the polynuclectide or as a probe for detecting the polynuclectide. The polynuclectides ADM01316-ADM03758 are useful in gene therapy, for developing a diagnostic marker or medicines for regulating their expression and activity, or as a target of gene therapy. The proteins ADM03759-ADM06201 encoded by the polynuclectides are useful as pharmaceutical agents. The present sequence represents a cDNA sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                  R, Tamechika
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                                                                                                                                                                                                                                                                                                                                     Ishii S;
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                                                                                                               ss; gene; human; gene therapy; diagnostic marker; pharmaceutical.
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                                                                                                                                                                                                                                                                                                                                    Otsuki T, Wakamatsu A, Sato H,
Hio Y, Otsuka K, Nagai K, Irie
Otsuka M, Nagahari K, Masuho Y;
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Pred. No. 0;
0; Mismatches
                                                                                 the invention SEQ ID NO:575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 575; 305pp; English
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                                                                                                                                                                                                                                                                         22-MAR-2002; 2002JP-00137785.
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                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                  Sugiyama T,
                                                                                                                                                                                                                                                                                                                                                    Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
                                                                                                                                                                                                                                                                                                                                                                                                   2003-723558/69.
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Best Local Similarity
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                                                                                                                                                Homo sapiens
                                                    20-MAY-2004
                                                                                                                                                                                                            24-SEP-2003.
                                                                                   Human cDNA
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                    TATAAGAGTCTTACTAGAAATTTGGCATCTAGAAATCTTGCTCCAAAAGGGGAGAAATTCA
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CCTGTTACAGACAATGCTAATGCAAGAATGAAGGCACATGTACGACGTGGAACAGCATTC
                                                                             TATAAGAGTCTTACTAGAAATTTGGCATCTAGAAATCTTGCTCCAAAAGGGAGAAATTCA
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/*tag= a
/product= "DYXC1 protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                This invention relates to a novel isolated human gene DYXC1 that is functionally related to dyslexia, more particularly it describes single nucleotide polymorphisms thought to predispose an individual in to developing dyslexia. This is a neurological disorder with a genetic basis (DYXC1 has been isolated to chromosome 15q21), which manifests itself as a specific reading disability. Specifically, DYXC1 is can be useful in study of brain processes such as reading, phonological processing, rapid naming and verbal short-term memory. Accordingly, the present invention describes methods and materials for analysing allelic variations in the DYXC1 gene, and also provides DYXC1 as an antigen for the production of antibodies used in the diagnosis of dyslexia. This polynucleotide sequence is the chimpanzee DYXC1 cDNA homologous to the human DYXC1 gene
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                                                                                                                                                                                                                                                                          New isolated, purified DYXC1 nucleic acid for studying brain processes, e.g. reading, phonological processing, rapid naming or verbal short-term memory, or for diagnosing dyslexia or assessing the predisposition to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAAAACTATCTGAAGGTCAACTTTCCTCCATTTTTATTTGAGGCATTTCTTTATGTGTCCC
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                                                                                                                                                                            Kaminen N;
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Pred. No. 0;
0; Mismatches 5
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                                                        12-FEB-2003; 2003WO-FI000110.
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Matches 1210; Conservative
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                                               ACTAAAAAACTTACACAAGGCTATTGAAGATTCTAAGGCACTGGAATTATTGATGCC
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                                                                                                                                                                                                                                                                                                                                                                                          New isolated, purified DYXC1 nucleic acid for studying brain processes, e.g. reading, phonological processing, rapid naming or verbal short-term memory, or for diagnosing dyslexia or assessing the predisposition to
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                                                                                                                                                                                                                                                                                                                                                                                                          This invention relates to a novel isolated human gene DYXC1 that is functionally related to dyslexia, more particularly it describes single duccleotide polymorphisms thought to predispose an individual in to developing dyslexia. This is a neurological disorder with a genetic basis (DYXC1 has been isolated to chromosome 15q21), which manifests itself as a specific reading disability. Specifically, DYXC1 is can be useful in study of brain processes such as reading, phonological processing, rapid naming and verbal short-term memory. Accordingly, the present invention describes methods and materials for analysing allelic variations in the DYXC1 gene, and also provides DYXC1 as an antigen for the production of antibodies used in the diagnosis of dyslexia. This polynucleotide
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                                                                                                                                                                                                                                                                                            isolated, purified DYXC1 nucleic acid for studying brain processes, reading, phonological processing, rapid naming or verbal short-term ory, or for diagnosing dyslexia or assessing the predisposition to
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                                                                                                                                                                                                                  Kaminen
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99.1%; Pred. No. 0;
ive 0; Mismatches
               "DYXC1 protein"
                                                                                                                                                                                                                                                                                                                                                                                Claim 29; Page 123-124; 135pp; English.
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                                                                                                                 2003WO-F1000110
                                                                                                                                                12-FEB-2002; 2002US-0355782P.
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Matches 1246; Conservative
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                                                 WO2003068814-A1
                                                                                                                                                                                                                                                                                                                   e.g. reading,
                                                                                                                 12-FEB-2003;
                                                                                21-AUG-2003
                                                                                                                                                                                                                                                                                                                                                 dyslexia.
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The invention relates to 971 novel human cDNA sequences (ADC29919-ADC30899) and the polypeptides they encode (ADC30890-ADC31860). The invention also relates to nucleic acid sequences over 19% identical with the novel human cDNAs. The invention additionally encompasses expression vectors and host cells comprising a nucleic acid of the invention; the recombinant production of a polypeptide of the invention; an antibody against a polypeptide of the invention; and methods of polypeptides of the invention; and methods of adentifying a compound which binds to a polypeptide of the invention. The invention further discloses methods of peventing, treating or analorating a medical condition; % its comprising polymucleotide probes analorating a medical condition; % its comprising polymucleotide probes analorating and cathods for the identification of compounds that modulate the invention; methods for the identification of compounds that modulate the expression or activity of the polymucleotide and/or polypeptide; and 767 contigs sequences corresponding to the consoled by the contigs (ADC31861-ADC32627) and the polymucleotides encoded by the contigs (ADC33861-ADC33384). The nucleic acids and polypeptides of the invention are useful in diagnostics, drug screening, forensics, gene mapping, in the identification of muteations responsible for genetic disorders or other traits, for assessing biodiversity, and in producing many other types of data and products dependent on DNA and amino acid sequences. They are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or cancer. The nucleic acids may also be used as hybridisation probes or primers, and in the recombinant production of a protein. The polypeptides are also useful in generating antibodies, as molecular weight markers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polynucleotide and polypeptide useful for diagnosing, preventing or treating conditions such as neurodegenerative diseases, anemias, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and as food supplements. The present sequence represents a human contig
sequence used in an example of the invention. Note: The sequence data for
this patent did not form part of the printed specification, but was
obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         data and products dependent on DNA and amino acid sequences. They are also used for treating diseases such as Parkinson's disease, Alzheimer's disease and other neurodegenerative diseases, anaemia, platelet
antiulcer; osteopathic; immunosuppressive; antiinflammatory; cytostatic;
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                                                                                                                                                                                                                                                                                                                                                                             Wehrman
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                                                                                                                                                                                                                                                                                                                                                                          Wang J,
Wang Z, W
                                                                                                                                                                                                                                                                                                                                                                          Xue AJ, Zhao QA,
Ma Y, Asundi V,
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                         gene therapy; chromosome 15q21.3; ss.
                                                                                                                                                                                                                                                                                                                                                                          Tang TY, Zhang J, Ren F, Xi
Zhou P, Ghosh M, Wang D, Mi
Haley-Vicente D, Drmanac RT;
                                                                                                                                                                                                                             24-SEP-2002; 2002WO-US030474.
                                                                                                                                                                                                                                                                           24-SEP-2001; 2001US-0324631P.
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Best Local Similarity 100.
Matches 524; Conservative
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P-PSDB; ADC32883.
                                                                                                                                                                                                                                                                                                                            (HYSE-) HYSEQ INC
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                                                                             Homo sapiens
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120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA.
                                    703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, 88, sequencing by hybridisation, SBH, expressed sequence tag; EST; genome mapping; biodiversity; genetic disorder.
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                                                                                   763
                                                                                                                                                      241 AAGTAGCAGAAGAGGAGGGGCTACACAACAAGCTGAGGCACGAAGAGCAATGAATA 300
301 CTGACATAGCTGAACTTTGCGATTTAAAAGAAGAAGAAAAGAAACCCAGAATGGTTGAAGG
                                                                                                                                                                                                                                       TAGCCATAAGACTAAATAATAAGATGCCACTATTGTATTTGAACCGGGCTGCTTGCCACC
                                                            121 ATTCAGAAAATATATTTACTGAGAAGTTAAAGGAAGACAGTATTCCTGCTCCTCGCTCTG
                                                                                                                                                                               ATAAAGGAAACAAATTGTTTGCAACGGAAAACTATTTGGCAGCTATCAATGCATATAATT
                                                                                  TIGGCAGTATTAAAATCAACTTTACCCCTCGAGTATTCCCAACAGCTCTTCGTGAATCAC
                                                                                                                                AAGTAGCAGAAGAAGGAGGAGGTACACAAACAAGCTGAGGCACGAAGAGCAATGAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jones LW;
                                      644 ATTCAGAAATATATTTACTGAGAAGTTAAAGGAAGACAGTATTCCTGCT
                                                                                                                                                                                                                                                                                                                       1004 TAAAACTAAAAACTTACACAAGGCTATTGAAGATTCTTCTAAG 1047
                                                                                                                                                                                                                                                                                                                                             524
                                                                                                                                                                                                                                                                                                                                  Dickson MC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 22675; 44pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                         ACH35463 standard; cDNA; 488
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(STAC/)
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41.5%; Score 524; DB 10; 100.0%; Pred. No. 1e-239; ive 0; Mismatches 0;

Length 608;

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1 TTCAGAGAGAAGAGAAATTATGTCAAAAAGAAAAGGAAATTAAAGAAGAAGAAAAAAA 60

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524 TTCAGAGAGAGAAATTATGTCAAAAAGAAAAGCAAATTAAAGAAGAAGAAAAAAA

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determined by the technique of SBH (sequencing by hybridisation). Also determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polymucleotide. The nucleic acid sequences corresponding to a reading frame of the novel polymucleotide. The nucleic acid sequences corresponding to identifying expressed genes or for physical mapping of the human genome, in forensise, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protain, or in generating antisease DNA or RNA. The purified polypeptide is useful for generating antisbodies specific for it. The present sequence is useful for generating antisbodies specific for it. The present sequence is useful and isolated DNA/EST sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ss; sequencing by hybridisation; SBH; expressed sequence tag; {\rm EST}_i mapping; biodiversity; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCGTCAGAGACACGGACGTGTTCTGCACGGAAAACTATCTGAAGGTCAACTTTCCTCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTTTATTTGAGGCATTTCTTTATGCTCCCATAGACGATGAGAGCAGCAAAGGTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                         80 GCGTCAGAGACACGGACGTGTTCTGCACGGAAAACTATCTGAAGGTCAACTTTCCTCCAT
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                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                 Length 488;
                                                                                                                                                                                                                                                                                                                            Sequence 488 BP; 141 A; 105 C; 126 G; 116 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                 4.1e-145;
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                                                                                                                                                                                                                                                                                     segdata.uspto.gov/sequence.html?DocID=20030073623
                                                                                                                                                                                                                                                                                                                                                               25.8%; Score 326; DB 9;
                                                                                                                                                                                                                                                                                                                                                                         100.0%; Prec. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AATACGCACTAAGTGTCATGATGAAG 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AATACGCACTAAGTGTCATGATGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACH23091 standard; cDNA; 458 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human adult ovary cDNA #1471.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JUL-2001; 2001US-00918995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JUL-2001; 2001US-00918995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 100.
nes 326; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (DRMA/) DRMANAC R T. (LABA/) LABAT I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US2003073623-A1.
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                                                                                                                                                                                                                                                                                                                                                                                     Best Loca
Matches
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The inversion traces, appearing as ACH12789-ACH5081, whose sequence we determined by the technique of SBH (sequencing by hybridisation). Also determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polymucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (EST) for dentifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antibodies specific for it. The present sequence is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data for this patent did not form part of the printed specification, but was contained in electronic formet directly from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GACTAAATAATAAGATGCCACTATTGTATTTGAACCGGGCTGCTTGCCACCTAAAACTAA 1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                 New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated polynucleotide comprising any one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         249 CTGAACTTTGCGATTTAAAAGAAGAAGAAAGAACCCAGAATGGTTGAAGGATAAAGGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      369 GACTAAATAAGATGCCACTATTGTATTTGAACCGGGCTGCTTGCCACCTAAAACTAA 428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             773 AAGAGGAGGAGTGGCTACACAAACAAGCTGAGGCACGAAGAGCAATGAATACTGACATAG
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                                                                            Jones LW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 458;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 458 BP; 170 A; 86 C; 97 G; 102 T; 0 U; 3 Other;
                                                                          Dickson MC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 270; DB 9; Le
Pred. No. 2.3e-118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding novel human diagnostic protein #5822.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          segdata.uspto.gov/seguence.html?DocID=20030073623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21.4%; Scc...
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1013 AAAACTTACACAAGGCTATTGAAGATTCTT 1042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         458
                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 10303; 44pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAS70018 standard; cDNA; 1383 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 270; Conservative
STACHE-CRAIN EDICKSON M C. JONES L W.
                                                                            Drmanac RT, Labat I,
                                                                                                               WPI; 2003-615964/58.
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(STAC/) (DICK/) (JONE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
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(first entry)

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ds; human; DYXC1; dyslexia; neurological disorder; chromosome 15q21; reading disability; phonological processing; rapid naming; verbal short-term memory.
                                                                 Human DYXC1 DNA, chromosomal gene region nucleotides 50001-100000.
                                                                                                                                                                                   WO2003068814-A1.
                                                                                                                                                         Homo sapiens
                                      20-NOV-2003
                                                                                                                                                                                                               21-AUG-2003
           ADB16927;
                                                                                                                                                                                                                                                                                                                               Kere J,
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                                                                                                                                                                                                                                                                                                                                                      The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal cativity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders of polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess blodiversity and to produce other types of data and products dependent on DNA and anno acid sequences. AbS64197-AAS94564 represent novel human diagnostic coding sequences. AbS64197-AAS94564 represent novel human diagnostic patent did not appear in the printed specification, but was obtained in electronic format directly from MIPO at the sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  172 GACGATGAGAGCAGCAAAGATTGGGAATGACACCATTGTCTTCACCTTGTATAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             709 GACGATGAGGAGCAAGGAAAGATTGGGAATGACACCATTGTCTCCTTGTATAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGAATTAGAGAAAAATCTATTTTACAAGCACAAGAGAGCAAAAGAAGCTACAGAAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                         New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1383;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.6%; Score 197; DB 5; Length 13
100.0%; Pred. No. 1.8e-83;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 5822; 103pp; English.
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                                                                                                                                                                                      Tang YT;
                                                                                                              31-MAR-2000; 2000US-00540217
23-AUG-2000; 2000US-00649167
                                                                                   30-MAR-2001; 2001WO-US008631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        al Similarity 100.
197; Conservative
                                                                                                                                                                                                               WPI; 2001-639362/73.
P-PSDB; ABG05831.
                                                                                                                                                                                      Liu C,
                                                                                                                                                         (HYSE-) HYSEQ INC
                            WO200175067-A2
                                                                                                                                                                                                                                                                                                      biodiversity.
  Homo sapiens
                                                                                                                                                                                      Drmanac RT,
                                                        11-0CT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention relates to a novel isolated human gene DXXC1 that is functionally related to dyslexia, more particularly it describes single nucleotide polymorphisms thought to predispose an individual in to developing dyslexia. This is a neurological disorder with a genetic basis (DYXC1 has been isolate to chromosome 15g21), which manifests itself as a specific reading disability. Specifically, DYXC1 is can be useful in study of brain processes such as reading, phonological processing, and escribes methods and materials for analysing allelic variations in the DYXC1 gene, and also provides DYXC1 as an antigen for the production of antibodies used in the diagnosis of dyslexia. This polynucleotide is the partial genomic sequence of the human DYXC1 chromosomal region
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                                                                                                                                                                                                                                                              New isolated, purified DYXC1 nucleic acid for studying brain processes, e.g. reading, phonological processing, rapid naming or verbal short-term memory, or for diagnosing dyslexia or assessing the predisposition to dyslexia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      404 AGATTGAAGAAGAAGAGGAAAAAAAATAGAAGATATGAAAGAAAATGAACGGATAAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 49806 BP; 12975 A; 10105 C; 10577 G; 15977 T; 0 U; 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.6%; Score 184; DB 9; Length 49806; 99.6%; Pred. No. 2.8e-77;
                                                                                                                                                                      Kaminen N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                      Taipale M, Nopola-Hemmi J,
                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 27; Page 69-83; 135pp; English.
12-FEB-2003; 2003WO-FI000110.
                                                      12-FEB-2002; 2002US-0355782P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (nucleotides 50001-100000)
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Best Local Similarity 99.6
Matches 234; Conservative
                                                                                                                   (LICN ) LICENTIA LTD
                                                                                                                                                                                                                                WPI; 2003-646482/61.
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RESULT 14 ADB16928

ADB16927 standard; DNA; 49806 BP.

RESULT 13 ADB16927 ID ADB , expressed sequence tag, secreted protein, cDNA isolation, chromosome mapping; ss.

Giordano J;

Duclert A,

99US-0122487P

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New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures.
                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 34573; 71pp + Sequence Listing; English
                                           Human secreted protein 5' EST, SEQ ID NO: 34573.
                                                                                                                                                                                                          21-FEB-2000; 2000EP-00200610.
                                                                                                                                                                                                                                                                                               Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                           WPI; 2000-500381/45.
                                                                                                                                                                                                                                                                  (GEST ) GENSET
                                                                                         gene therapy;
                                                                                                                      Homo sapiens
                                                                                                                                                EP1033401-A2
                                                                                                                                                                                                                                     26-FEB-1999;
                06-OCT-2000
                                                                                                                                                                             06-SEP-2000.
                                                                         Human;
 This invention relates to a novel isolated human gene DYXC1 that is functionally related to dyslexia, more particularly it describes single functionally related to dyslexia, more particularly it describes single developing dyslexia. This is a neurological disorder with a genetic basis (DYXC1 has been isolated to chromosome 15q1), which manifests itself as a specific reading disability. Specifically, DYXC1 is can be useful in study of brain processes such as reading, phonological processing, rapid naming and verbal short-term memory. Accordingly, the present invention describes methods and materials for analysing allelic variations in the DYXC1 gene, and also provides DYXC1 as an antigen for the production of antibodies used in the diagnosis of dyslexia. This polymucleotide is the partial genomic sequence of the human DYXC1 chromosomal region (nucleotides 100001-150000) of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                               New isolated, purified DYXC1 nucleic acid for studying brain processes, e.g. reading, phonological processing, rapid naming or verbal short-term memory, or for diagnosing dyslexia or assessing the predisposition to
                                                                                                                ds; human; DYXCl; dyslexia; neurological disorder; chromosome 15q2l; reading disability; phonological processing; rapid naming; verbal short-term memory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 49939 BP; 13786 A; 10910 C; 11127 G; 14116 T; 0 U; 0 Other;
                                                                                    Human DYXC1 DNA, chromosomal gene region nucleotides 100001-150000.
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100.0%; Pred. No. 2e-63;
cive 0; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 27; Page 83-97; 135pp; English
ADB16928 standard; DNA; 49939
                                                                                                                                                                                                                                                                12-FEB-2003; 2003WO-FI000110
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                                                        (first entry
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                                                        20-NOV-2003
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The present sequence is one of a large number of 5' ESTS derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTS were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oilgo-dT primed CDNA libraries. Such ESTS are not well suited for isolating conn sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. S' ESTS are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTS are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCCTCAAAGGCGTGTGGGTCAGAGACACGGACGTGTTCTGCACGGAAAACTATCTGAAGG 124
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Pred. No. 1.5e-49;
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Matches 155; Conservative

Best Local Similarity

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AAC30498 standard; cDNA; 164 BP

AAC30498

(9)28)

(otqsu) Anole Blank (uspto)

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1. .1993
/gene="BKN1"
/note="wildtype gene occasionally disrupted by chromosomal
transleation breakpoint"
369. .1631
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Taipale, M., Kaminen, M., Nopola-Hemmi, J., Haltia, T., Myllyluoma, B., Lyytinen, H., Muller, K., Kaaranen, M., Lindsberg, P.J., Hannla-Jouppi, K. and Kere, J. A candidate gene for developmental dyslexia encodes a nuclear tetratricopeptide repeat domain protein dynamically regulated in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A gene disrupted by translocation breakpoint in chromosome 15q21 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 100 (20), 11553-11558 (2003)
22882828
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Taipale, M. and Kere, J.
Taipale, M. and Kere, J.
Direct Submission
Submitted (17-3AN-2001) Finnish Genome Center, University
Helsinki, Tukholmankatu 2, Helsinki 00014, Finland
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                          AF337549 RKN1 (EKN1) mRNA, complete cds. AF337549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. 1993
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="15"
/map="15q21.2"
                                                                                                                                                                                                                                                                               ALIGNMENTS
AY178610S5
AY178583S7
AY178681S7
AY178610S7
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AY17859284
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AY178593S8
AY178610S9
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BC062564 Homo sapi
AR413597 Sequence
AX970431 Sequence
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AC022083 Homo sapi
CQ685075 Sequence
AC021668 Homo sapi
AC03355 Homo sapi
AC03355 Homo sapi
AX178584 Pan trog1
AX178587 Pan trog1
AX178596 Pan panis
AX178602 Gorilla g
AX178605 Gorilla g
AX178605 Gorilla g
AX178611 Pongo pyg
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         GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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Pongo pyg Sequence

Gorilla g

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                     /protein_id="AAL73230.1"
/db_xref="GI:18478648"
        codon_start=1
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GAGTGGCTACAAACAAGCTGAGGCACGAAGAGCAATGAATACTGACATAGCTGAACTT 1208
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: BP 1347046-A 575 24-SEP-2003;
Research Association for Biotechnology
Location/Qualifiers
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0; Mismatches
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1002

Euteleostomi;

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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
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Hopkins, R.F., Jordan, H., Moore, T., Wax, S. I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
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Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Morseran, K.J., Male, M.J., Gunarane, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.M.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Samilus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.,
Generation and initial analysis of more than 15,000 full-length
                                                                                                                 961 AATAAGATGCCACTATTGTATTTGAACCGGGCTGCTTGCCACCTAAAAACTAAAAACTTA 1020
                                                                                                                                                                                                                                                                                                                                       BC062564 1inear PRI 28-NOV-2003 Homo sapiens dyslexia susceptibility 1 candidate 1, mRNA (cDNA clone MGC:70618 IMAGE:5163101), complete cds.
                                                                                                                                    TGCGATTTTAAAAGAAGAAGAAGCCCAGAATGGTTGAAGGATAAAGGAAACAAATTG 942
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Submitted (24-NOV-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_msc@ndpari.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspl,R.,
                                   WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
bDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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                                                                           Clone distribution: MGC clone distribution information can be found through the I.M.A.G. R. Consortiun/LiML at: http://image.llnl.gov Series: IRAK Plate: 135 Row: a Column: 3 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 18677736. I.ocation/Qualifiers
                                                                            be found
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/note="p23; Region: homolog to co-chaperone p23"
/db_xref="CDD:cd00237"
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ive 0; Mismatches
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                                                                                            ACTGAGAAGTTAAAGGAAGACAGTATTCCTGCTCCTCGCTCTGGTTGGCAGTATTAAAATC
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Pred. No. 1.2e-196;
); Mismatches 0;
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Sequence 1234 from patent US 6639063.
AR413597
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Edwards,J.-B.D.M., Jobert,S. and Giords
EST's and encoded human proteins
Patent: US 6639063-A 1234 Z8-OCT-2003;
Location/Qualifiers
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/mol_type="genomic DNA"
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100.0%; Pred
0; M
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323 GGGTGTTGACAAAGAGATGATGCAAAGAATTAGAGAAAATCTATTTACAAGCACAAGA 382
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BD109150.1

JP 2002010789-A/1227.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

BMmmalla; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 489)

Edwards,J.B.D.M., Jobert,S. and Giordano,J.E.

BST and encoded human protein

Patent: JP 2002010789-A 1227 15-JAN-2002;
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JP 2002010789-A/1227
15-JAN-2002
15-JAG-2000
05-AUG-2000 US 60/147499
US 60/147499
US ADUTIST DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE
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PC C12N5/19, C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21,
PC C12N5/10, C12P21/02, C12P21/08, C12Q1/68, C12N15/00, C12N15/00, CC EST and encoded human protein
FH Key
FT CDS
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/organism="Homo sapiens"
/mol type="genomic DNA"
/db_xref="taxon:9606"
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                                         326
                                                                                                                                                                                                                                    GAGAGCAAAAGAAGCTACAGAAGCAAAAGCTGCAGCAAAGCGGGAAGATCAAAAATACGC 386
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                           CACCATTGTCTTCACCTTGTATAAAAAAGCGGCCATGTGGGAGACCCTTTCTGTGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Dumas Milne Edwards, J.B., Jobert, S. and Giordano, J.Y.
ESTs and encoded human proteins
Patent: EP 1104808-A 1234 06-JUN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         489 bp DN Sequence 1234 from Patent EP1104808. AX970431

    .489
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'note="sequence data generated from subcloned PCR product"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 AAGGTCAACTTTCCCCCATTTTTTATTTGGGCATTTCTTTATGCTCCCATAGACGATGAG 180
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31516 CCACTABAGCATTGGAAGCCTGGAAAGAATATCAAAGAAAAGCTGAGGAGCAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             404 AGATTGAAGAAGAAGAGGAAAAAAATAGAAGATATGAAAGAAAATGAACGGATAAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                       49 ATGCCTCTTCAGGTTAGCGATTACAGCTGGCAGCAGAGGAGGAGGAGGAGCTGCGGCTTTCTGTCT
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                                                                                                                                                                                                                                                            18.6%; Score 235; DB 9; Length 114149; 100.0%; Pred. No. 8.8e-109; tive 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Compositions and methods relating to osteoarthritis Patent: WO 02070737-A 30001 12-SEP-2002; Chondrogene Inc. (CA)
                                                                                                                                                  /note="overlap with RP11-458H3, AC012674"
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/note="overlap with RP11-420M1, AC012378"
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CQ685075
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Matches 214; Conservative
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Direct Submission
Submitted (26-JAN-2000) Multimegabase Sequencing Center, University
of Washington, PO BOX 357730, Seattle, WA 98195, USA
3 (bases 1 to 114149)
Rowen, L., Madan, A., Qin, S., Baradarani, L., Birditt, B., Bloom, S.,
Burke, J., Dors, M., Fleetwood, P., Kaur, A., Madan, A., Nesbitt, R.,
                                                                                                                                                                                                                                        PRI 12-MAY-2001
Submitted (12-MAY-2001) Multimegabase Sequencing Center, Institute for Systems Biology, 4225 Roosevelt Way NE, Suite 200, Seattle, WA
                                                                                                                                                                                                                                     AC022083 114149 bp DNA linear PRI 12-MAY-20
Homo sapiens chromosome 15 clone CTD-2137J4 map 15q21.3, complete
                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
Rowen, L., Madan, A., Qin, S., Baradarani, L., Birditt, B., Bloom, S., Burke, J., Dors, M., Fleetwood, P., Kaur, A., Madan, A., Nesbitt, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (Dases I to 114149)
Rowen, L., Madan, A., Qin, S., Abbasi, N., Baradarani, L., Birditt, B., Bloom, S., Dors, M., Dickhoff, R., Fleetwood, P., Harrison, G., James, R., Kaur, A., Madan, A., Owen, M.P., Ratcliffe, A., Shaffer, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /map="15q21.3"
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/note="This clone overlaps RP11-178D12 AC013355,
RR11-458H3 AC012674 and RP11-42ON1 AC012378. Data from
overlapping BACS were added and the consensus sequence
determined from CTD-2137J4 to the extent possible."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Note: Data from overlapping clones AC013355 [Drafting center: UWMSC], AC012674 [Drafting center: BCM] and AC012378 [Drafting center: UWMSC] were added for finishing.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pate, D. and Hood, L. Sequencing of human chromosome 15 D15S146-D15S117 region
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Web site: http://chroma.mbt.washington.edu/msg_www
Contact: leerowenosystemsbiology.org
Contact: Summary Statistics
Sequencing vector: pUC18; L08752
Chemistry: Dye-terminator Big Dye; 90% of reads
Chemistry: Dye-primer Big Dye; 10% of reads
Assembly program: Phrap; version 0.990399
                                                                                                            443 ACTAAGTGTCATGAAGATTGAAGAAGAAGAGGGGAAAAAATAG 489

    47896
/note="oerlap with RP11-178D12, AC013355"

                                                                                   Center: Multimegabase Sequencing Center
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/db_xref="taxon:9606"
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Direct Submission
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Homo sapiens chromosome 15 clone RP11-13306 map 15, LOW-PASS
BEQUENCE SAMPLING.
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://fp.genome.washington.edu/RM/RepeatMasker.html
http://fp.genome.washington.edu/RM/RepeatMasker.html
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
Contact: Project Information
Center project name: 11276
Center clone name: 133_0_6
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845: gap of 100 bp
1576: contig of 731 bp in length
1676: gap of 100 bp
2410: contig of 734 bp in length
2510: gap of 100 bp
3332: contig of 722 bp in length
3332: gap of 100 bp
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 15, clone RP11-13306
   229 AGCAGCAAAGCAAAGATTGGGAATGACACCATTG 262
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AC021668.4 GI:13488020
HTG; HTGS_PHASE0.
Homo sapiens (human)
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2 (bases 1 to 43886)
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/clone_lib="RPCI human BAC library 11"
Cnote="This clone overlaps RP11-139H15 AC018926 and Cnote="This AC022083. Data from overlapping BACs were added and the consensus sequence determined from RP11-178D12 to the extent possible."
                                                                                                             Submitted (09-NOV-1999) Multimegabase Sequencing Center, University of Washington, PO BOX 357730, Seattle, WA 98195, USA 3 (bases 1 to 151133)
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121540. .121935
/note="sequence data generated from subcloned PCR product"
                                                                                                                                                                                                                                        Submitted (15-JUN-2001) Multimegabase Sequencing Center, Institute for Systems Biology, 4225 Roosevelt Way NE, Suite 200, Seattle, WA 98105, USA
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                                     Rowen, L., Madan, A., Qin, S., Abbasi, N., Baradarani, L., Birditt, B., Bloom, S., Dors, M., Dickhoff, R., Harrison, G., James, R., Madan, A., Owen, M.P., Ratcliffe, A., Shaffer, T. and Hood, L. Direct Submission
                                                                                                                                                                      Rowen, L., Madan, A., Qin, S., Baradarani, L., Birditt, B., Bloom, S., Burke, J., Dors, M., Fleetwood, P., Kaur, A., Madan, A., Nesbitt, R., Pate, D. and Hood, L.
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Web site: http://chroma.mbt.washington.edu/msg_www
Contact: leerowendsystemsbiology.org
------Summary Statistics
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Chemistry: Dye-terminator Big Dye; 90% of re
Chemistry: Dye-primer Big Dye; 10% of reads
Assembly program: Phrap; version 0.990399
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/note="low quality data"
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/db_xref="taxon:9606"
/chromosome="15"
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Rowen,L., Madan,A., Qin,S., Baradarani,L., Birditt,B., Bloom,S., Burke,J., Dors,M., Fleetwood,P., Kaur,A., Madan,A., Nesbitt,R., Pate,D. and Hood,L.
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42322: gap of 100 bp
42355: contig of 733 bp in length
43155: gap of 100 bp
43155: contig of 731 bp in length.
                                       0 bp
735 bp in length
                                                                                                                                                                                                                                                                                                                        contig of 735 bp in length
gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /map="15"
/clone="RP11-13306"
/clone_lib="RPC1-11 Human Male BAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.6%; Score 184; DB 2;
.larity 99.6%; Pred. No. 1.3e-82;
Conservative 0; Mismatches 1;
100 bp
of 720 bp i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Homo sapiens"
                   contig of 73 gap of 100 h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic_DNA"
/db_xref="taxon:9606"
/chromosome="15"
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AC013355.7 GI:14456641
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AUTHORS
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is contig of 944 bp in length contig of 915 bp in length contig of 1234 bp in length contig of 1234 bp in length contig of 1234 bp in length gap of unknown length length contig of 1175 bp in length gap of unknown length length contig of 1175 bp in length gap of unknown length length contig of 914 bp in length gap of unknown length length contig of 914 bp in length gap of unknown length length contig of 914 bp in length gap of unknown length length contig of 1013 bp in length gap of unknown length length contig of 1013 bp in length gap of unknown length length contig of 914 bp in length gap of unknown length gap of unknown length gap of unknown length gap of unknown length length gap of unknown length gap of unknown length gap of unknown length length gap of unknown length gap of unk
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208181 bp DNA linear HTG 04-JUN-2000
HOMO sapiens chromosome 15 clone RP11-460A24 map 15q21, LOW-PASS
SEQUENCE SAMPLING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 208181)

Rowen, L., Madan, A., Oloin, S., Abbasi, N., Baradarani, L., Birditt, B., Bloom, S., Dors, M., Dickhoff, R., Fleetwood, P., Harrison, G., Kaur, A., Madan, A., Nesbitt, R., Shaffer, T. and Hood, L. Sequencing of human chromosome 15 DISS146-DISS117 region Unpublished

2 (bases 1 to 208181)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rowen, L., Madan, A., Oin, S., Abbasi, N., Baradarani, L., Birditt, B., Bloom, S., Dors, M., Dickhoff, R., Fleetwood, P., Harrison, G., James, R., Kaur, A., Madan, A., Owen, M.P., Ratcliffe, A., Shaffer, T.
                            * NOTE: This record contains 191 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://chroma.mbt.washington.edu/msg_www
Contact: leerowen@systemsbiology.org
------ Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequencing vector: pUC18; L08752
Chemistry: Dye-terminator Big Dye; 90% of reads
Chemistry: Dye-primer Big Dye; 10% of reads
Assembly program: Phrap; version 0.990399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       contig of 856 bp in length
gap of unknown length
contig of 861 bp in length
gap of unknown length
contig of 973 bp in length
gap of unknown length
gap of unknown length
gap of unknown length
gap of unknown length
contig of 1067 bp in length
contig of 1087 bp in length
gap of unknown length
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AC016527.2 GI:8247792
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                                                                                                                                                                                                                                                                                                             Homo sapiens (human)
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AUTHORS
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JOURNAL
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PRI 02-OCT-2003

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3 (bases 1 to 147)

Kaminen, N. and Kere, J.

Direct Submission

Submitted (13-NOV-2002) Department of Medical Genetics, University of Helsinki, PO Box 63, Haartmaninkatu 8, Helsinki FIN-00014,
                                                                                                                                                                                                                                                                                                                                      Eukaryota Mortacoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan. 1 (bases 1 to 147).
Taipale, M., Kaminen, N., Nopola-Hemmi, J., Haltia, T., Myllyluoma, B., Lyytinen, H., Muller, K., Kaaranen, M., Lindsberg, P.J., Hannla-Jouppi, K. and Kere, J.
Ramnla-Jouppi, K. and Kere, J.
A candidate gene for developmental dyslexia encodes a nuclear tetratricopeptide repeat domain protein dynamically regulated in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 GTCAACTTTCCTCCATTTTTATTTGAGGCATTTCTTTATGCTCCCATAGACGATGAGAGC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 147)
Kaminen, N. and Kere, J.
EKNI gene orthologs in chimpanzee, pygmy chimpanzee, gorilla and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 100 (20), 11553-11558 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 147;
                                                                                                                                                                                  linear
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Pan troglodytes EKN1 (EKN1) gene, exon 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.6%; Score 147; DB 9; 1
100.0%; Pred. No. 2.1e-63;
ive 0; Mismatches 0;
                                                                CCATGTGGGAGCCTTTCTGTGACGGGTG 22509

    147/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"

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PRI 02-OCT-2003 184 AGCAAAGCAAAGATTGGGAATGACACCATTGTCTTCTCTTGTATAAAAAGAAGCGGCC 243 61 AGCAAAGCAAAAGATTGGGAATGACACCATTGTCTTCACCTTGTATAAAAAAGAAGCGGCC 120 9 1 Greaactricercertritatricagecarrictritatgerecearagaege linear 147 bp DNA
Pan troglodytes EKN1 (EKN1) gene, exon 6.
AY178587
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182 GCAGCAAAGCAAAGATTGGGAATGACACCATTGTCTTCACCTTGTATAAAAAGAAGGG

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Kaminen,N. and Kere,J.
Direct Submission
Submitted (13-NOV-2002) Department of Medical Genetics, University
of Helginki, PO Box 63, Haartmaninkatu 8, Helsinki FIN-00014,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        637 GGGAGAAATTCCAGAAAATATTTTACTGAGAAGTTAAAGGAAGACAGTATTCCTGCTCCT 696
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                                                                Bukaryosio, Verezoa, Chordata, Craniata, Vertebrata, Euteleostomi, Bukaryosio, Mammalia, Buthoria, Primates, Catarrhini, Hominidae, Pan. I (bases I to 14).

Taipale, M., Kaminen, N., Nopola-Hemmi, J., Haltia, T., Myllyluoma, B., Lyytinen, H., Miller, K., Kaaranen, M., Lindsberg, P.J., Mamnula-Jouppi, K. and Kere, J.

A candidate gene for developmental dyslexia encodes a nuclear tetratricopeptide repeat domain protein dynamically regulated in
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Taipale, M., Kaminen, N., Nopola-Hemmi, J., Haltia, T., Myllyluoma, B., Lyytinen, H., Muller, K., Kaaranen, M., Lindsberg, P.J., Mannla-Zouppi, K. and Kere, J.

A candidate gene for developmental dyslexia encodes a nuclear tetratricopeptide repeat domain protein dynamically regulated in
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Kaminen, N. and Kere, J.
EKN1 gene orthologs in chimpanzee, pygmy chimpanzee, gorilla and
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/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
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Saminen, N. and Kere, J.
Direct Submission
Submitted (13-NOV-2002) Department of Medical Genetics, University
of Helsinki, PO Box 63, Haartmaninkatu 8, Helsinki FIN-00014,
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Kaminen, N. and Kere, J.
EKNI gene orthologs in chimpanzee, pygmy chimpanzee, gorilla and
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Proc. Natl. Acad. Sci. U.S.A. 100 (20), 11553-11558 (2003)
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Matches 147; Conservative 0; Mismatches 0;
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APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
ITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REPERENCE: GENNER. 1054PR2
CURRENT FILING DATE: 2000-07-21
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 1234
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US-09-556-002-36
US-09-949-016-17297
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US-09-949-016-17651
US-09-949-016-12620
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Patent No. 6639063
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; LOCATION: 57..488
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/cgn2_6/ptodata1/ina/5A_COMB.seq:*
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/cgn2_6/ptodata1/ina/6B_COMB.seq:*
/cgn2_6/ptodata1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata1/ina/PCTUS_COMB.seq:*
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                          version 5.1.6
- 2005 Compugen Ltd.
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seq length: 200000000
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Gaps

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Result Š. 146 202 322

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ORGANISM: Homo sapiens
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                                                                                                                               US-09-513-999C-34573
; Sequence 34573, Application US/09513999C
; Sequence 34573, Application US/09513999C
; GENERAL INPORMATION:
; APPLICANT: Duclert, A.
; APPLICANT: Duclert, A.
; APPLICANT: Glocdano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT FILING DATE: 2000-22-4
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SEQ ID NO 34573
; LENGTH: 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 30814, Application US/09513999C

Sequence 30814, Application US/09513999C

Patent No. 6783961

GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Duclert, A.

APPLICANT: Giordano, J.Y.

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

PILE REFERENCE: 59.US2.REG

CURRENT APPLICATION NUMBER: US/09/513,999C

CURRENT FILING DATE: 1099-02-24

PRIOR APPLICATION NUMBER: US 60/122,487

PRIOR FILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681

SEQ ID NO 30874
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                                            443 ACTAAGTGTCATGATGAAGATTGAAGAAGAAGAGAGAGAAAAAATAG 489
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// LCCATTON: 128

// OTHER INFORMATION: b=a or c or t

US-09-513-999C-34573
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OTHER INFORMATION: y=c or
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100 AATTTAGCCATAAGACTAAATAAGATGCCACTATTGTATTTGAACCGGGCTGCTTGC 159
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APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Monath, Roadoh
APPLICANT: Mohamath, Roadoh
TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF
TITLE OF INVENTION: LONG CANCER AND METHODS FOR THEIR USE
TITLE OF INVENTION: LONG CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.475c1
CURRENT APPLICATION NUMBER: US/09/370,838
CURRENT AILING DATE: 1999-08-09
EARLIER FILING DATE: 1999-04-02
SOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH. 1316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 313;
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8.6%; Score 109; DB 4; I
Best Local Similarity 100.0%; Pred. No. 4.3e-42;
Matches 109; Conservative 0; Mismatches 0;
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US-09-513-999C-30874
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                                                                                                                                                                                                                  LOCATION: 85
OTHER INFORMATION: w=a
                        LOCATION: 82
OTHER INFORMATION: r=a
                                                                                                                                                                                            NAME/KEY: misc_feature
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NAME/KEY: misc_feature
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NAME/KEY: misc_feature
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Sequence 12670, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAPTITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
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Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REPERENCE: CL001307
CURRENT PFLICATION NUMBER: US/09/949,016
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REPERENCE: CLOOL307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR PAPLICATION NUMBER: 60/241,755

PRIOR PAPLICATION NUMBER: 60/241,755

PRIOR PAPLICATION NUMBER: 60/231,498

PRIOR PAPLICATION NUMBER: 60/231,498

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTHARE: FastSEQ for Windows Version 4.0

LENGTH: 118143
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100.0%; Pred. No. 18;
iive 0; Mismatches
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Best Local Similarity 100.
Matches 20; Conservative
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Matches 20; Conservative
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; ORGANISM: Human
US-09-949-016-16513
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ORGANISM: Human
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Patent No. 6747137

Patent No. 6747137

Patent No. 6747137

Patent No. 6747137

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT PILING DATE: 1998-02-12

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NOS: 28208
                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Mohamath, Raodoh
APPLICANT: Mohamath, Raodoh
APPLICANT: Hondresson, Robert A.
APPLICANT: Benson, Darin R.
APPLICANT: Benson, Darin R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
FILE REPERENCE: 210121.475C10
CURRENT APPLICATION NUMBER: US/09/854,133
CURRENT FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 735
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 30
LENGTH: 1316
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100.0%; Pred. No. 2;
tive 0; Mismatches 0; Indels
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18;
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Pred. No.
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2.09-949-016-17196
; Sequence 17196, Application US/09949016
; Patent No. 6812339
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       408 TGAAGAAGAGAGAGAAAAA 429
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100.0%; Pre
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Patent No. 6759508
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Matches 22; Conservative
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Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapien
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COUNTRY:
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; Sequence 11853, Application US/09513999C
; Sequence 11853, Application US/09513999C
; Patent No. 678361
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Glordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 678361
; FILE REFERENCE: 59.US2.RG
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR PLILNG DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SQ ID NO 11853
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54;
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100.0%; Pred. No. 54;
tive 0; Mismatches 0
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ilarity 100.0%; Pred. No. 54;
Conservative 0; Mismatches
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
ESQ ID NO 12670
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RESULY 11

Sequence 45, Application US/08343443B

Patent No. 5968734

GENERAL INFORMATION:
APPLICANT: Aurias, Alain
APPLICANT: Delattre, Olivier
APPLICANT: Melot, Thomas
APPLICANT: Peter, Martine
APPLICANT: Peter, Martine
APPLICANT: Peter, Martine
APPLICANT: Ptomas
APPLICANT: Thomas
APPLICANT: Thomas
APPLICANT: Thomas
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US-09-513-999C-11853
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Best Local Similarity 100."
Matches 19; Conservative
                                                                                                                                                         ; TYPE: DNA; Candida albicans
US-09-248-796A-12670
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LOCATION: 241
OTHER INFORMATION: s=g or
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LOCATION: 242
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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Sequence 389, Application US/09540236

Fatent No. 66739104

Patent No. 66739104

GENERAL INFORMATION.

APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.2005-001

CURRENT APPLICATION NUMBER: US/09/540,236

CURRENT APPLICATION NUMBER: 2000-04-04

NUMBER OF SEQ ID NOS: 3840

SEQ ID NO 389
                                                               CHROMOSOME 22 INVOLVED IN RECURRENT CHROMOSOMAL TRANSLATIONS ASSOCIATED WITH THE DEVELOPMENT OF CANCEROUS TUMORS, AND NUCLEIC ACIDS OF FUSION RESULTING FROM SAID TRANSLOCATIONS
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NUCLEIC ACID CORRESPONDING TO A GENE OF
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100.0%; Pred. No. 54;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compactible
OCMFUTER: IBM PC compactible
OPERATING SYSTEM: PC-DOSG
SOFTWARE: AEDIT 1.0 DOS text editor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/343,443B
FILING DATE: 18-NOV-1994
CLASSIFICATION BATA:
APPLICATION NUMBER: PCT/FR93/00494
FILING DATE: 19-MAY-1993
RIPING APPLICATION DATA:
APPLICATION NUMBER: PCT/FR93/00494
FILING DATE: 19-MAY-1992
ATJORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 999.6121P
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 19,763
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
TITLE OF INVENTION: UNCLEIC ACID CORI
TITLE OF INVENTION: UNCLEIC ACID CORI
TITLE OF INVENTION: TRANSLATIONS ASSO
TITLE OF INVENTION: TRANSLATIONS ASSO
TITLE OF INVENTION: TRANSLOCATIONS
NUMBER OF SEQUENCES: 129
CORRESPONDENCE ADDRESS:
ADDRESSEE: Weiser & Associates
STREET: 230 South Fifteenth Street
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                565 AAAGAAGGAAGAAAAAA 583
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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; ORGANISM: M.catarrhalis
US-09-540-236-389
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Best Local Similarity
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Best Local Similarity
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0; Gaps

0; Indels

0; Mismatches

19; Conservative

Matches

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Search completed: July 8, 2005, 12:07:45 Job time : 248 secs
                        US-09-949-016-51133/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-949-016-51133
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Sequence 23804, Application US/09949016

Batent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-00-03

PRIOR PILING DATE: 2000-00-03

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NOS: 207012

SEQ ID NOS: 207012
                                                                                                                                                     Sequence 23803, Application US/09949016

Patent No. 6812339
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CL00130,
CURRENT APPLICATION NUMBER: US/09/949,016
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54;
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                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-08

PRIOR FILING DATE: 2000-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 23803

LENGTH: 601
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                        383 TAAAAGAAGAAGAAAGAA 401
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848 TAAAAGAAGAAGAAAGAA 866
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                                                                                                              RESULT 13
US-09-949-016-23803
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US-09-949-016-23803
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ORGANISM: Human
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(uspto) Angle Blank (uspto)

Gorilla g Pongo pyg Sequence

Sequence Sequence

Pan trogl
Pan panis
Gorilla g
Pongo pyg
Pan trogl
Pan panis
Pan panis
Gorilla g
Gorilla g
Pongo pyg
Pongo pyg

AY178604 Gorilla
AY178613 Pongo I
AX9185101 Sequent
BD050544 Sequent
BD050544 Sequent
AY178589 Pan tra
AY178589 Pan par
AY178584 Pan tra
AY178596 Pan par
AY178602 Gorilla
AY178605 Gorilla
AY178609 CORILLA
AY178609 Pan par
AY178609 Pan par
AY178609 Pan pan

Pan panis Gorilla g

Pongo pyg Mus muscu Pan panis

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1. ...1993
/gene="EKN1"
/note="wildtype gene occasionally disrupted by chromosomal
translocation breakpoint"
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1 (bases 1 to 1993)
1 Taipale, M., Kaminen, M., Nopola-Hemmi, J., Haltia, T., Myllyluoma, B., Lyytinen, H., Miller, K., Kaaranen, M., Lindsberg, P.J., Hannia-Jouppi, K. and Kerej.
A candidate gene for developmental dyslexia encodes a nuclear tetratricopeptide repeat domain protein dynamically regulated in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 1993)
Taipale,M. and Kere,J.
A gene disrupted by translocation breakpoint in chromosome 15q21
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Taipale, M. and Kere, J.
Taipale, M. and Kere, J.
Direct Submission
Submitted (17M-2001) Finnish Genome Center, University
Helsinki, Tukholmankatu 2, Helsinki 00014, Finland
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/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/chromosome="15"

/map="15q21.2"
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BD05654
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AK095201 Homo sapi
BC062564 Homo sapi
BC062564 Homo sapi
BC07575 Kenopus 1
AR413597 Sequence
AK970431 Sequence
BD109150 EST and e
CQ685075 Sequence
BC065881 Danio rer
CR387522 Gallus ga
CR389904 Gallus ga
AC022083 Homo sapi
AC01355 Homo sapi
AC016597 Homo sapi
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- 2005 Compugen Ltd.
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Copyright (c) 1993
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PRI 15-JUN-2004

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Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S., Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R., Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and
GAGTGGCTACAAACAAGCTGAGGCACGAAGAGCAATGAATACTGACATAGCTGAACTT 1208
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                         TGCGATTTAAAAGAAGAAGAAAGAACCCAGAATGGTTGAAGGATAAAGGAAACAAATTG
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); Mismatches 1;
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Patent: EP 1347046-A 575 24-SEP-2003;
Research Association for Biotechnology
Location/Qualifiers
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100.0%; Pred. No. 3e-237;
ive 0; Mismatches 0;
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Matches 1263;
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TITLE
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/protein_id="BAC04498.1"

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/translatato="MPLQVSDYSWQTKTAVPLSLPLKGVCVRDTDVFCTENYLKVNF

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I AELCDLKEEEKNPEWLKDKGNKLPATENYLAAINAYNLAI RLNNKMPLLYLNRAACH
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                                                                                                                                 Score 1047.4; DB 9; Length
Pred. No. 5e-195;
0; Mismatches 1; Indels
                                                                                                                                 82.9%;
llarity 99.9%;
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Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Altschul, S.F., Zeeberg, B., Buetcow, K.H., Schaefer, C.F., Bhat, N.R.,
Altschul, S.F., Zeeberg, B., Buetcow, K.H., Schaefer, C.F., Bhat, N.R.,
Hopking, R.F., Jordan, H., Morce, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casawant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
McKernan, K.J., Mallahy, S.J., Bossk, S.A., McEwan, P.J.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Glbbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Schmutz, J., Myers, R.M.,
Generation and mouse cDNA sequences
M.D. Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                          1002
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                                                                                                                                                                                                                                                                                     BC062564
Homo sapiens dyslexia susceptibility 1 candidate 1, mRNA (cDNA clone MGC:70618 IMAGE:5163101), complete cds.
                                                                             TITGCAACGGAAAACTAITIGGCAGCTATCAATGCATATAAATTTAGCCATAAGACTAAAT 960
883 TGCGATTTAAAAGAAGAAGAAAGAACCCAGAATGGTTGAAGGATAAAGGAAACAAATTG 942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1468)
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Submitted (24-NO-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaithersburg, Maryland;
Web aite: http://www.nisc.nih.gov/
Contact: nisc.mgc@nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Akhter,N., Ayele,K. Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Districh,N. L., Granite,S., Gunta,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
                                                                                                                              cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIH-MGC Project URL: http://mgc.nci.nih.gov
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                               1021 CACAAGGCTATTGAAGATTCTTCTAAGGC 1049
1063 CACAAGGCTATTGAAGATTCTTCTAAGGC 1091
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BC062564.1 GI:38565951
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Homo sapiens
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Strausberg, R.
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L. (Dates 1 to 1944).

Strausberg, R.L., Feingold, B.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S. I., Wang, J., Haieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Soares, M.B., Banaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
McKernan, K.J., Malek, J.A., Gunaranne, P.H., Richards, S.,
Worley, K.C., Hale, S., Carcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Glbbs, R.A.,
Fahey, J., Helton, B., Ketteman, M., Madon, A., Schmutz, J., Myers, R.M.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BC026462 1946 bp mRNA linear ROD 29-JUN-2004 Mus musculus dyslexia susceptibility 1 candidate 1 homolog (human), mRNA cone MGC:31465 IMAGE:4483015), complete cds.
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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukamialia; Butheria; Rodentia; Sciurognathi; Muridae; Mus
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ACTAGAAATTTGGCATCTAGAAATCTTGCTCCAAAAGGGAGAAAATTCAGAAAATATATTT
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IPTEKLKEDSI PAPRSOKSIKINFTRYVPPTALRESOVAEBEEWLHKOAARANNTD
IAELCDLKEEEKNPEWLKOKGNKLFATENYLAAINAYNLAIRLNNKMPLLYLNRAVCH
                                                                                                                 be found
                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="MCC:70618 IMAGE:5163101"
/tissue_type="Colon, Kidney, Stomach, adult, whole pooled"
/clone_lib="NIH MGC_116"
/lab_host="DH108"
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PPFLFEAFLYAPIDDESSKAKIGNDTIVFTLYKKEAAMWETLSVTGVDKEMMQRIREK
Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.
                                                                                                            Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at: http://image.llnl.gov Series: IRAK Plate: 135 Row: a Column: 3 This clone was selected for full length sequencing because it passed the following selected for full length sequencing because it
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/note="p23; Region: homolog to co-chaperone p23"
/db_xref="CDD:cd00237"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             product="dyslexia susceptibility 1 candidate
/protein id="AAH62564.1"
/db_xref="G1:38565952"
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                                                                                                                                                                                                                                                                            'organism="Homo sapiens"
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Contact: MGC help desk
Contact: GGC help desk
Tissue Procurement: Gilbert Smith, Ph.D.
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site:
http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mod@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
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/protein id="AAH26462.1"
/db_xref="GI:20071434"
                                                                                                                                                                                                                                                                                                                                                                                                          Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 44 Row: b Column: 9 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                            Direct Submission
Submitted (02-APR-2002) National Institutes of Health, Mammalian
Submitted (02-APR-2002) National Cancer
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db.crail.t.pd/m.//db.crafe="taxon:10090" /db.crafe="taxon:10090" /clone="MGC:31465 IMAGE:4483015" /tissue type="Mammary tumor. Metallothionien-TGF alpha model: 10 month old virgin mouse. Taken by biopsy." /clone lib="MCI CGAP_Mam1" /lab_host="DH10B"
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0; Mismatches 245;
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/db_xref="LocusID:67685"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
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       mouse cDNA sequences
L. Acad. Sci. U.S.A.
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Klausner, R.D., Collins, F.S., Wagner, L., Schemen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, B., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.
Butfard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marza, M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (19-JUL-2004) National Institutes of Health, Xenopus Gene Collection (XGC), National Institute of Child Health and Human Development, 6100 Executive Boulevard, Room 4B01, Rockville, MD 20892-7510, USA
                                                                                                                                                                                                                                       BC077575 2004 NRNA linear VRT 12-OCT-2004 Xenopus laevis dyslexia susceptibility 1 candidate 1, mRNA (cDNA clone MGC:83582 IMAGE:5079663), complete cds.
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                                                                                 1182 TTGTATGTTGAAGGCTTGCAAGATTATGAAGCTGCACTTAAGATTGACCCAGCCAACACA 1241
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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Klein,S.L., Strausberg,R.L., Wagner,L., Pontius,J., Clifton,S.W. and Richardson,P.
Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                    1201 ATTGTACAAATTGATGCTGAGAATTCGGAATGTAATTCAAGGAACAGAACTAAAATCT
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Email: cgapberremail.nih.gov
Tissue Procurent: Martha Rebbert, Steven L. Klein, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
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Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Xenopus laevis
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIANL at: http://image.llnl.gov Series: IRAK Plate: 153 Row: a Column: 7 This clone was because it full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
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PPFLFRAFLFAPIDDSTSSAKIGNGVILFNLHKKEPAVWDLTLAHNEKEEMOKIREN
AVKEQEKAROETKAKAERKENEKYELBYTWKIDEVERKRIEDVERKRIEELEELE
KWKEKQRIOKLAGCKOIROKKOIROBNENKALHITGSLKHCSTATTVQNDRTINVKOKEKI
LPPTRSTGGIQIQFTPRVFPFALRESRVAEBEEWLHKQAEARRATNTVDLGLEDLTEE
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EDSSKALELLTPPVPGNASARIKAHVRRGTAFCELELYVEGLODYBAALKI DPTNQNM
KSDAEKIRRVIQSSLPDIERGIMLDIKDL."
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Best Local Similarity 63.5%; Pred. No. 5.9e-85;
Matches 789; Conservative 0; Mismatches 423;
                                                                                                                                                                                                                                                                                                                                                                          /organism="Xenopus laevis"
/mol_type="mRNA"
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/clone="MGC:83582 IMAGE:5079663"
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/protein id="AAH77575.1"
/db_xref="G1:50603774"
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clone Tib="NICHD_XGC_OO1"
lab host="DH108"
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/codon start=1
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/tanslation="MPLQYSDYXWQOTKTAVFLSLELKGVCVRDTDVFCTENYLKVNF
PPFLFEAFLYAPIDDESSKAXIGNDT1VFTLYKKEAAAW#ETLSVTGVDKEMMQRIREK
SILQAQERAKEATEAKAAAAREBDQKYALSVMWKIEEBERKKI"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Patent: EP 1104808-A 1234 06-JUN-2001;
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Pred. No. 1.3e-74;
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/note="unnamed protein product"
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Sequence 1234 from Patent EP1104808.
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/db_xref="taxon:9606"
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Best Local Similarity 99.8%;
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                                                       ATTGTACAAATTGATGCTGAGAAGATTCGGAATGTAATTCAA 1242
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1 (bases 1 to 489)
Edwards,J.-B.D.M., Jobert,S. and Giordano,J.-Y.
Edwards and encoded human proteins
Patent: US 6639063-A 1234 28-OCT-2003;
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                  CTGCCCCTCAAAGGCGTGTGCGTCAGAGACACGGACGTGTTCTGCACAGGAAAACTATCTG
                                                                                                                                                           117 CTGCCCCTCAAAGGCGTGTGCGTCAGAGACACGGACGTGTTCTGCACGGAAAACTATCTG
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                                                                  AGCAGCAAAGCAAAGATTGGGAATGACACCATTGTCTTCACCTTGTATAAAAAAGGAGCG
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  Mismatches

    464
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

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Edwards,J.B.D.M., Jobert,S. and Giordano,J.E.
Bar and encoded human protein
Patent: JP 2002010789-A 1227 15-JAN-2002;
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JP 2002010789-A/1227
JP 2002010789-A/1227
07-5406-2000 JP 2000280989
05-AUG-1999 US 60/147499
JEAN BAPUTIST DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE
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C12N1/21,
PC C12N5/10,C12P21/02,C12P21/08,C12Q1/68,C12N15/00,C12N15/00,C12N15/00
CC EST and encoded human protein
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                                                                                                           CTGCCCCTCAAAGGCGTGTGCGTCAGAGACACGGACGTGTTCTGCACGGAAAACTATCTG
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Pred. No. 1.3e-74;
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/organism="Homo sapiens"
/mol type="genomic DNA"
/db_xref="taxon:9606"
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JP 2002010789-A/1227.
Homo sapiens (human)
Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BC065881 1443 bp mRNA linear VRT 30-JUN-2004
Danio rerio zgc:77853, mRNA (cDNA clone MGC:77853 IMAGE:7002321),
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Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth
Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
GAAAAATCTATTTTACAAGCACAAAAGAAGCAAAAAGAAGCTACAGAAGCAAAAGCTGCA 360
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Submitted (126-JAN-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                         GCCATGTGGGAGACCCTTTCTGTGACGGGTGTTGACAAAGAGATGATGCAAAGAATTAGA
                                                                                                                                                                                                                                                                                                               Email: cgapbs-remail.nih.gov
Tissue Procurement: Len Zon, Harvard
CDNA Library Preparation: Open Biosystems
CDNA Library Arrayed by: Hogiens T.M.A. G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
                                                                                                                                                                                                                                                                                    GCAAAGCGGGAAGATCAAAATACGCACTAAGTGTCATGATGAAGATTGAA 411
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Contact: MGC help desk
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Danio rerio
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AUTHORS
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KEYWORDS
SOURCE
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   Josh Moran, Ryan Morin,
                                                                                                                                                                                                      Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLML at: http://image.llnl.gov Series: IRAK Plate: 147 Row: p Column: 24
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Mori
Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu,
Parvaneh Saeedi, JR Santose, Angelique Schnerch, Ursula Skalska,
Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie
Schein, Asim Siddiqui, Rob Holt, Marco Marra.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="hypothetical protein zgc:77853"
/protein_id="AAH65881.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Danio rerio"
/mol type="mRNA"
/db_xref="taxon:7955"
/clone="MGC:77853 IMAGE:7002321"
/tissue type="Whole, adult zebrafish"
/clone lib="NHH ZGC_10"
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/db_xref="LocusID:402988"
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Archosauria, Aves, Neognathae, Galliformes, Phasianidae,
Phasianinae, Gallus.
                                                                                                                                         sequencing project
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                                                                    AGAACCAGCACATGACAACAACGGTTCCTCAGAAATAAAGCATGCAAACACTTCA
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Gallus gallus (chicken) Gallus gallus Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

GI:46240281

CR387522.1

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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This sequence is from the BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST cDNA collection, from a library constructed by Elizabeth Bosch. cDNA was prepared from RNA extracted from hearts, normalised, and poly A-trimmed. ECORINOLI cut cDNA was then ligated into the vector. Vector: pBlueecript II KS(+); Site_1: ECORI; Site_2: NotI Host: Escherichia coli DH10B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1030 ATTGAAGATTCTTCTAAGGCACTGGAATTATTGATGCCACCTGTTACAGACAATGCTAAT 1089
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1 (bases 1 to 761)
Boardman, P.B., Bonfield, J.K., Brown, W.R.A., Carder, C., Chalk, S.B., Croning, M.D.R., Davies, R.M., Francis, M.D., Grafham, D.V., Hubbard, S.J., Humphray, S.J., Hunt, P.J., Maddison, M., McLaren, S.R., Niblett, D., Overton, I.M., Rogers, J., Scott, C.B., Taylor, R.G., Tickle, C. and Wilson, S.A.
Direct Submission
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                                                                                                                                                                                     Submitted (05-APR-2004) Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. B-mail enquiries: chickest@bms.umist.ac.uk
BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST Gallus gallus cDNA
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Gallus gallus finished cDNA, clone ChEST271nl3.
CR389904
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Pred. No. 2.8e-48;
0; Mismatches 110;
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/mol_type="mENA"
/strain="Compton Line 151
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/clone="ChEST505n19"
/clone_lib="CSEQCHN60"
/dev_etage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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Best Local Similarity 76.8%;
Matches 364; Conservative (
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CR389904
LOCUS
DEFINITION
ACCESSION
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Direct Submission
Submitted (26-JAN-2000) Multimegabase Sequencing Center, University of Washington, PO BOX 357730, Seattle, WA 98195, USA
3 (bases 1 to 114149)
Rowen,L., Madan,A., Qin,S., Baradarani,L., Birditt,B., Bloom,S., Burke,J., Dors,M., Fleetwood,P., Kaur,A., Madan,A., Nesbitt,R., Direct Submission
Submitted (12-MAY-2001) Multimegabase Sequencing Center, Institute Submitted (12-MAY-2001)
                                                                                                                                                                                                    ACU22083 114149 bp DNA linear PRI 12-MAY-2001
Homo sapiens chromosome 15 clone CTD-2137J4 map 15q21.3, complete
sequence.
           for Systems Biology, 4225 Roosevelt Way NB, Suite 200, Seattle, WA
                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (human)
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mamaalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dasses 1 to 114149)
Rowen, L., Madan, A., Qin, S., Baradarani, L., Birditt, B., Bloom, S.,
Burke, J., Dors, M., Fleetwood, P., Kaur, A., Madan, A., Nesbitt, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rown, L., Madan, A., Qin, S., Abbasi, N., Baradarani, L., Birditt, B., Bloom, S., Dors, M., Dickhoff, R., Fleetwood, P., Harrison, G., James, R., Kaur, A., Madan, A., Owen, M.P., Ratcliffe, A., Shaffer, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="CTD-2137J4"
/clone_lib="Cal Tech human BAC library D"
/clone_This clone overlaps RP11-178D12 AC013355,
RP11-458H3 AC012674 and RP11-420M1 AC012378. Data from overlapping BACs were added and the consensus sequence determined from CTD-2137J4 to the extent possible."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Note: Data from overlapping clones AC013355 [Drafting center: UWMSC], AC012674 [Drafting center: BCM] and AC012378 [Drafting center: UWMSC] were added for finishing.

Location/Qualifiers
                                                                                                     On May 12, 2001 this sequence version replaced gi:13621222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Multimegabase Sequencing Center
Center code: UWMSC
Web site: http://chroma.mbt.washington.edu/msg_www
Contact: lerrowendsystemsbiology.org
Sequencing vector: pUC18; L08752
Chemistry: Dye-terminator Big Dye; 90% of reads
Chemistry: Dye-terminator Big Dye; 10% of reads
Assembly program: Phrap; version 0.990399
                                                        Pate, D. and Hood, L. Sequencing of human chromosome 15 D15S146-D15S117 region Unpublished
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/note="oerlap with RP11-178D12, AC013355"
18530. .18640
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/mol type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /map="15q21.3"
                                                                                                                                                                                                                                                                                                                 AC022083.6 GI:14029048
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                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

1. (basea 1 to 1133)

Boardman, P. E., Bonfield, J.K., Brown, W.R.A., Carder, C., Chalk, S.E., Croning, M.D.R., Davies, R.M., Francis, M.D., Grafham, D.V., Miblett, D., Overton, I.M., Rogers, J., Maddison, M., McLaren, S.R., Tickle, C. and Wilson, S.A.

Tickle, C. and Wilson, S.A.
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                                                                                                                                                                                                                                                                                                                   Cambridgeshire,
                                                                                                                                                                                                                                                                                                                 Submitted (19-ARR-2004) Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: chickest@bms.umist.ac.uk
BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST Gallus gallus CDNA
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al Similarity 66.4%; Pred. No. 8.8e-44;
395; Conservative 0; Mismatches 200; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Gallus gallus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db xref="taxon:9031"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          location/Qualifiers
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/strain="Layer"
GI:46428549
                                          gallus (chicken)
                                                                                                                                                                                                                                                                                                                                                                                             sequencing project
                                                                    Gallus gallus
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Center: Whitehead Institute/ MIT Center for Genome Research
On Mar 29, 2001 this sequence version replaced gi:11612359. All repeats were identified using RepeatMasker: Smit, A-R-A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                              * NOTE: This record contains 53 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
the record is updated, the accession number will
* be preserved.
                                                                                                                                                                            Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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  note="sequence data generated from subcloned PCR product"
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1 (bases 1 to 43886)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens chromosome 15, clone RP11-13306
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Submitted (19-JAN-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                      398 TGATGAAGATTGAAGAAGAAGAGGAAAAAAATAGAAGATATGAAAGAAATGAAACGGA
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/note="low quality data"
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/note="overlap with RP11-458H3, AC012674"
/note="overlap with RP11-420M1, AC012378"
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                                                                                                                                                                                                                                                                         Query Match 19.1%; Score 241; DB 9; Best Local Similarity 92.7%; Pred. No. 3.2e-37; Matches 253; Conservative 0; Mismatches 20.
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AC021668.4 GI:13488020
HTG; HTGS_PHASE0.
Homo sapiens (human)
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39729: contig of 721 bp in length

39729: contig of 721 bp in length

40548: contig of 719 bp in length

40648: gap of 100 bp

41383: contig of 719 bp in length

41483: gap of 100 bp

42222: contig of 739 bp in length

43322: gap of 100 bp

43322: contig of 739 bp in length

43055: contig of 739 bp in length
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Search completed: July 8, 2005, 03:29:22 Job time : 5662 secs

398 TGATGAAGATTGAAGAAGAAGAGAAAAAAAATAGAAGATATGAAAGAAAATGAACGGA

Query Match
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Best Local Similarity 92.3%; Pred. No. 6.9e-37;
Matches 252; Conservative 0; Mismatches 21; Indels 0;

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us-10-681-199-1.rng

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Copyright (c) 1993 - 2005 Compugen Ltd.
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Description	Adb16964 Human DYX Adb16965 cDNA sequ	Adb16939 Pygmy chi Adb16933 Chimpanze	Adb16935 Gorilla D	Adc30210 Human nov	Adm01890 Human cDN	Adb16924 cDNA sequ	Adc32116 Human nov	Ach35463 Human end	Ach23091 Human adu	Aas70018 DNA encod	Adb16927 Human DYX	Aac26799 Human sec	Aac30498 Human sec	Adb16928 Human DYX	Abl33958 Human imm	Abl33404 Human imm	Acd92384 Human col
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                                                                                                                                      This invention relates to a novel isolated human gene DYXC1 that is functionally related to dyslexia, more particularly it describes single developing dyslexia. This is a neurological disorder with a genetic basis (DYXC1 has been isolated to chromosome 15q21), which manifests itself as a specific reading disability. Specifically, DYXC1 is can be useful in etudy of brain processes such as reading, phonological processing, rapid naming and verbal short-term memory. Accordingly, the present invention describes methods and materials for analysing allelic variations in the DYXC1 gene, and also provides DYXC1 as an antigen for the production of antibodies used in the diagnosis of dyslexia. This polynuclectide represents the coding sequence of human DYXC1 CDNA of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                     This invention relates to a novel isolated human gene DYXC1 that is functionally related to dyslexia, more particularly it describes single duccleotide polymorphisms thought to predispose an individual in to developing dyslexia. This is a neurological disorder with a genetic basis (DYXC1 has been isolated to chromosome 15q21), which manifests itself as specific reading disability. Specifically, DYXC1 is can be useful in study of brain processes such as reading, phonological processing, rapid naming and verbal short-term memory. Accordingly, the present invention describes methods and materials for analysing allelic variations in the DYXC1 gene, and also provides DYXC1 as an antigen for the production of antibodies used in the diagnosis of dyslexia. This polynucleotide is the CDNA sequence of the wild type human DYXC1 mRNA of the invention.
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                                                                                                                                                                                                                                                           New isolated, purified DYXC1 nucleic acid for studying brain processes, e.g. reading, phonological processing, rapid naming or verbal short-term memory, or for diagnosing dyslexia or assessing the predisposition to
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gene; se; chimpanzee; DYXC1; dyslexia; neurological disorder; reading disability; phonological processing; rapid naming; verbal short-term memory.
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                                                                                                                                                                      "DYXC1 protein"
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Pred. No. 1.7e-260;
0; Mismatches 9; Indels 0;
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                                                                                           gene; 88; gorilla; DYXC1; dyslexia; neurological disorder; reading disability; phonological processing; rapid naming; verbal short-term memory.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated, purified DYXC1 nucleic acid for studying brain processes, e.g. reading, phonological processing, rapid naming or verbal short-term memory, or for diagnosing dyslexia or assessing the predisposition to
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Pred. No. 1.8e-259;
0; Mismatches 12; Indels 0;
                                                                                                                                                                                                                 gene; ss; orangutan; DYXC1; dyslexia; neurological disorder; reading disability; phonological processing; rapid naming;
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                                                                                                                                                                                                                                                                                                                                ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to 971 novel human cDNA sequences (ADC29919-ADC30889) and the polypeptides they encode (ADC30890-ADC31860). The invention also relates to nucleic acid sequences over 99% identical with the novel human cDNAs. The invention additionally encompasses expression vectors and host cells comprising a nucleic acid of the invention; the recombinant production of a polypeptide of the invention; an antibody against a polypeptide of the invention; and methods of against a polypeptide of the invention; and methods of the invention invention which binds to a polypeptide of the invention. The invention further discloses methods of perventing, treating or amedical condition; kits comprising polymucleotide probes and invention; methods for the identification of compounds that modulate the invention; methods for the identification of compounds that modulate the invention; methods for the polymucleotide and/or polypeptide; and 767 contion; methods for the polymucleotide and/or polypeptide; and 767 contion; methods for the polymucleotide and/or polypeptide; and 767 contion; methods and polypeptides encoded by the contigs (ADC33628) ADC33394). The nucleic acids and polypeptides of the invention are identification of mutations responsible for genetic disorders or other traits, for assessing biodiversity, and in producing many other types of
New polynuclectide and polypeptide useful for diagnosing, preventing or treating conditions such as neurodegenerative diseases, anemias, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                molecular weight marker; food supplement; antiparkinsonian; nootroplc; neuroprotective; antianaemic; anticoagulant; thrombolytic; vulnerary; antiulcer; osteopathic; immunosuppressive; antiinflammatory; cytostatic; gene therapy; chromosome 15q21.3; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            biodiversity assessment; Parkinson's disease; Alzheimer's disease;
neurodegenerative diseases; anaemia; platelet disorder; wound; burns;
ulcers; osteoporosis; autoimmune disease; cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; diagnostic; drug screening; forensics; gene mapping;
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Wang Z, I
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                                                                                                                                                                                                                                                                                                                                                                                              Human novel cDNA sequence, SEQ ID NO:292
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                                                                                                                                                                                                                                                  ADC30210 standard; cDNA; 1641 BP
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also used for treating diseases such as Parkinson's disease. Alzheimer's disease and other neurodegenerative diseases, anaemia, platelet disease and other neurodegenerative diseases, anaemia, platelet cancer. The nucleis may also be used as hybridisation probes or primers, and in the recombinant production of a protein. The polypeptides are also useful in generating antibodies, as molecular weight markers, and as food supplements. The present sequence represents a specifically claimed human cDNA sequence of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
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100.0%; Pred. No. 2.9e-217;
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Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
Otsuka M, Nagahari K, Masuho Y;
 943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a novel human polynucleotide and the encoded polypeptide. A polynucleotide of the invention may have a use in gene therapy. An oligonicleotide of the invention ADM06202-ADM06773 is useful as a primer for synthesizing the polynucleotide or as a probe for detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are useful in gene therapy, for developing a diagnostic marker or medicines for regulating their expression and activity, or as a target of gene therapy. The proteins ADM03795-ADM06201 encoded by the polynucleotides are useful as pharmaceutical agents. The present sequence represents a
                                   TGCGATTTAAAAGAAGAAGAAGAAGAACCCAGAATGGTTGAAGGATAAAGGAAAAATTG
                                                                                                             AATAAGATGCCACTATTGTATTTGAACCGGGCTGCTTGCCACCTAAAACTAAAACTTA
GAGTGGCTACACAAACAAGCTGAGGCACGAAGAGCAATGAATACTGACATAGCTGAACTT
                      TGCGATTTAAAAGAAGAAGAAAGAACCCAGAATGGTTGAAGGATAAAGGAAACAAATTG
                                                                  TTTGCAACGGAAAACTATTTGGCAGCTATCAATGCATATAATTTAGCCATAAGACTAAAAT
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                                                                                                                                                                                                                                                                                                                                 gene therapy; diagnostic marker; pharmaceutical.
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                                                                                                                                                                                                                                                                                                          Human cDNA of the invention SEQ ID NO:575
                                                                                                                                                         CACAAGGCTATTGAAGATTCTTCTAAGGC
                                                                                                                                                                     CACAAGGCTATTGAAGATTCTTCTAAGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA sequence of the invention.
                                                                                                                                                                                                                                        ADM01890 standard; cDNA; 1559
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Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
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P-PSDB; ADM04333.
                                                                                                                                                                                                                                                                                                                                  gene; human;
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Query Match 82.9%; Score 1047.4; DB 11; Length 1559; Best Local Similarity 99.9%; Pred. No. 6.4e-217; Matches 1048; Conservative 0; Mismatches 1; Indels 0;

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               121 AAGGTCAACTTTCCTCCATTTTTATTTGAGGCATTTCTTTATGCTCCCATAGACGATGAG
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AGCAGCAAAGCAAAGATTGGGAATGACACCATTGTCTTCACCTTGTATAAAAAAGAAGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated, purified DYXC1 nucleic acid for studying brain processes, eg. reading, phonological processing, rapid naming or verbal short-term memory, or for diagnosing dyslexia or assessing the predisposition to dyslexia.
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                                                                                                                                                                                  gene; ss; mouse; DYXC1; dyslexia; neurological disorder; reading disability; phonological processing; rapid naming; verbal short-term memory; murine.
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                                                                                                                                                                                                                                                                                                                                                                    "DYXC1 protein"
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                                                                                                                                                mRNA
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                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                            sequence of the murine DYXC1
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                         ADB16924 standard; cDNA; 1697
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P-PSDB; ADB16925.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polynucleotide and polypeptide useful for diagnosing, preventing or treating conditions such as neurodegenerative diseases, anemias, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
                                                                                                                                                                       Human; diagnostic; drug screening; forensics; gene mapping; biodiversity assessment; Parkinson's disease; Alzheimer's disease; neurodegenerative disease; anaemia; platelet disorder; wound; burns; ulcers; osteoporosis; autoimmune disease; cancer; molecular weight marker; food supplement; antiparkinsonian; nootropic; eneuroporotective; antianeamic; anticoagulant; thrombolytic; vulnerary; antiulcer; osteopathic; immunosuppressive; antiinflammatory; cytostatic; gene therapy; chromosome 15q21.3; ss.
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Wang Z,
                                                                                                                                               Human novel cDNA contig sequence, SEQ ID NO:2198.
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Ma Y, Asundi V,
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Haley-Vicente D, Drmanac RT;
                                              ADC32116 standard; cDNA; 608
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Shosh M, Wang D,
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Zhou P, G
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and as food supplements. The present sequence represents a human contig sequence used in an example of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formed directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, 88, sequencing by hybridisation, SBH, expressed sequence tag, EST,
genome mapping, biodiversity, genetic disorder.
                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                              TAAAATATAAGAGTCTTACTAGAAATTTGGCATCTAGAAATCTTGCTCCAAAAGGGAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 ATTCAGAAAATTTTACTGAGAAGTTAAAGGAAGACAGTATTCCTGCTCCTCGCTCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 644 ATTCAGAAAATATATTTACTGAGAAGTTAAAGGAAGACAGTATTCCTGCTCCTCGCTCTG
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                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                Length 608;
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                                                                                                                                    Sequence 608 BP; 230 A; 103 C; 135 G; 140 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                              Score 524; DB 10; L
Pred. No. 1.1e-103;
                                                                                                                                                              41.5%; Scor.
100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                                                                                                                         Matches 524; Conservative
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                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                Query Match
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ACH23091;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                  18043 CDNA sequences, appearing as ACH12709-ACH56031, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polymucleotide. The nucleic acid sequences are reading frame of the novel polymucleotide. The nucleic acid sequences cresponding to are useful in diagnostics as expressed sequence tags (EST) for identifying expressed genes or for physical mapping of the human genome, in forensible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisease DNA or RNA. The purified polypeptide is useful for generating antisease DNA or RNA. The purified polypeptide is useful for generating antisease by sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCTTCACCTTGTATAAAAAAGAGGGCCATGTGGGGAGACCCTTTCTGTGACGGGTGTTG 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCTTCACCTTGTATAAAAAGAAGCGGCCATGTGGGAGACCCTTTCTGTGACGGGTGTTG 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAGAAGCTACAGAAGCAAAAGCTGCAGCAAAGCGGGAAGATCAAAAATACGCACTAAGTG 394
                                                                                                                 CDNA libraries, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95 ACGIGITCIGCACGGAAAACIAICIGAAGGICAACITTICCICCATTITIAITTGAGGCAT 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aagaagctacagaagcaaaagctgcagcaaagcgggaagatcaaaaatacgcactaagtg 387
                                                                                                                                                                                                          invention relates to an isolated polynucleotide comprising any one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28 adaccaadacrecegrerricrerererececercaagecercagegereagacacege 87
                                                                                                                               as hybridization probes, as oligomers for PCR, for chromosome and gene
mapping, in the recombinant production of protein, or in generating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35 AGACGAAGACTGCGGTCTTTCTGTCTCTCCCCTCAAAGGCGTGTGCGTCAGAGACACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                Jones LW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 9; Length 488;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 488 BP; 141 A; 105 C; 126 G; 116 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                Dickson MC,
                                                                                                                   polynucleotide sequences obtained from various
                                                                                                                                                                                                                                                                                                                                                                                                                 segdata.uspto.gov/sequence.html?DocID=20030073623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29.3%; Score 369.8; DB 9 99.5%; Pred. No. 2.4e-70; ive 0; Mismatches 2
                                                                                                                                                                                Claim 1; SEQ ID NO 22675; 44pp; English.
                                                                Stache-Crain B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCATGATGAGGAT 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similaricy
hes 371; Conservative
 LABAT I.
STACHE-CRAIN B.
DICKSON M C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCATGATGAAGCT
                                                                 Labat I,
                                                                                                                                                        antisense DNA or RNA.
                                                                                        WPI; 2003-615964/58
                                                                RT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  395
  (LABA/)
(STAC/)
                          (DICK/)
(JONE/)
                                                                  Ormanac
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  원
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ACH23091 standard; cDNA; 458 BP

RESULT 12 ACH23091 ID ACH2: XX

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The invention relates to an isolated polymucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polymucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (EST) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversities, or in identifying mutations cresponsible for genetic disorders and other traits. The nucleotide correction of the also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antibodies specific for it. The present sequence is useful for generating antibodies specific for it. The present sequence is one of the 3843 isolated CDNA/EST sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         818
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              819 GAATACTGACATAGCTGAACTTTGCGATTTAAAAGAAGAAGAAAAGAACCCCAGAATGGTT 878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA.
                                                                                                                     expressed sequence tag; EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAGAAATTCAGAAAATATATTTACTGAGAAGTTAAAGGAAGACAGTATTCCTGCTCCTCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jones LW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 458 BP; 170 A; 86 C; 97 G; 102 T; 0 U; 3 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dickson MC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seqdata.uspto.gov/sequence.html?DocID=20030073623
                                                                                                                     Human, 88; sequencing by hybridisation; SBH; e:
genome mapping; biodiversity; genetic disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 10303; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stache-Crain B,
                                                            Human adult ovary cDNA #1471.
                                                                                                                                                                                                                                                                                                                                                                                               30-JUL-2001; 2001US-00918995
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(first entry)
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Best Local Similarity 91.1'
Matches 368; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LABAT I.
STACHE-CRAIN E
DICKSON M C.
JONES L W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Labat I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-615964/58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DRMANAC R T.
                                                                                                                                                                                                                    Homo sapiens
13-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (DICK/)
(JONE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (DRMA/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (STAC/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LABA/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
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electronic format directly from WIPO at

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The invention relates to isolated polymuclectide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (FOR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymuclectides are also used in diagnostics as expressed sequence tags for identifying expressed care in diagnostics as expressed sequence tags for identifying expressed cartivity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supporting in tissue, as molecular weight markers and as a food stees expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The involving aberrant protein expression or biological activity. The collapseptide and polymuclectide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in
                                                                                                     354
                                                                  938
                                                                                                                                                                                    414
355 TAATTTAGCCATAAGACTAAATAATAAGATGCCACTATTGTATTTGAACCGGGCTGCTTG
                                                                                                     GAAGGATAAAGGAAACAAATTGTTTTGCAACGGAAAACTATTTGGCAGCTATCAATGCATA
                                                                                                                                          TAATTTAGCCATAAGACTAAATAATAAGATGCCACTATTGTATTTGAACCGGGCTGCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, chromosome mapping; gene mapping; gene therapy, forensic, food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                           CCACCTAAAACTAAAAACTTACACAAGGCTATTGAAGATTCTT 1042
                                                                                                                                                                                                                                                CCACCTAAAACTAAAAAACTTACACAAGGCTATTGAAGATTCTT 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding novel human diagnostic protein #5822.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 5822; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                  BP
                                                                                                                                                                                                                                                                                                                                                                AAS70018 standard; cDNA; 1383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                              TTTTACCACGCACGACGATGAGAGCAGCAAAGCAAAGATTGGGAATGACACCATTGTCTT
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                                                                                                             Gaps
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                                                                            DB 5; Length 1383;
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                                                                          19.4%; Score 245.2; DB 91.8%; Pred. No. 3e-43; ive 0; Mismatches :
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study of brain processes such as reading, phonological processing, rapid naming and verbal short-term memory. Accordingly, the present invention describes methods and materials for analysing allelic variations in the DYXCI gene, and also provides DYXCI as an antigen for the production of antibodies used in the diagnosis of dyslexia. This polynucleotide is the partial genomic sequence of the human DYXCI chromosomal region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss.
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                                                                                                                                                                                                                                                                            Sequence 49806 BP; 12975 A; 10105 C; 10577 G; 15977 T; 0 U; 172 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               398 TGATGAAGATTGAAGAAGAAGAGGAAAAAAATAGAAGATATGAAAGAAAATGAACGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures.
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sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dr primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures.
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           GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
                                                                                                                                                                                                                                                                                 34239544 segs, 19032134700 residues
                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                           OM nucleic - nucleic search, using sw model
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AK005832
BQ217312
BY705981
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CN478982
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CB297042
BF207765
CN429788
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BI517373
BU607404
BU567908
AK015345
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CK598370
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BE564350
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Maximum DB seq length: 2000000000
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1263
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9b_est2:*
9b_htc:*
9b_est3:*
9b_est4:*
9b_est6:*
9b_est6:*
9b_gs81:*
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812.6
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                                                                                                          Run on:
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CD107587
AGENCOURT 14021179 NIH MGC 179 Homo sapiens CDNA clone IMAGE:30368368 5', mRNA sequence.
1013 TAATAAGATGCCACTATTGTATTTGAACCGGGCTGCTTGCCACCTAAAAACTTAAAAAATT 1072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue type="Pituitary"
/lab host="DH10B-Ton A (T1 and T5 phage resistances)"
/lab host="DH10B-Ton A (T1 and T5 phage resistances)"
/clone_lib="NNH-MGC_179"
/note="Organ: brain; Vector: pCMV-SPORT6.1; Site_1: ECORV (destroyed); Site_2: Not1; Library is oligo-dT primed and directionally cloned (ECORV site is destroyed upon cloning). Average insert size 1.1 kb. Library was constructed by (Invitrogen). Note: this is a NIH_MGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137
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                                                                                                                                                                                                                                                                                             Homo sapiens
Mukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 844)

1 (bases 1 to 844)

NH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
Tissue Procurement: Dr. Michael Brownstein
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM431 row: a column: 17
High quality sequence stop: 634.
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                                    1020 ACACAAGGCTATTGAAGATTCTTCTAAGGC 1049
1073 ACACAAGGCTATTGAAGATTCTTCTAAGGC 1102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
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/clone="IMAGE:30368368"
                                                                                                                                                                                                                                         CD107587.1 GI:30760665
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AUTHORS
TITLE
JOURNAL
COMMENT
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                                                                                               Gaps
                                                         Length 1600;
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G
                                                       81.9%; Score 1034.8; DB 3
.larity 99.7%; Pred. No. 9.3e-215;
Conservative 0; Mismatches 2;
       /note="Vector: pDNR-LIB'
                                                                            Best Local Similarity
Matches 1047; Conser
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/mol_type="mRNA"
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/clone="IMAGE:30386203"
/lab host="DH10B-TON A (T1 and T5 phage resistances)"
/clone=lib="NIH MGC 180"
/clone=lib="Organ: Testis, Vector: pCMV-SPORT6.1; Site 1: Not1;
Site 2: ECGRV (destroyed); Library is oligo-dT primed and directionally cloned (ECGRV site is destroyed upon cloning). Average insert size 1.68 kb. Library was constructed by (Invitrogen). Note: this is a NIH_MGC Library.
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                                                                                                                                                                                                                                                                              Score 676.4; DB 6; Length 933;
Pred. No. 1e-136;
0; Mismatches 22; Indels 4
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High quality sequence stop: 6
Location/Qualifiers
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Best Local Similarity 96.5%;
Matches 723; Conservative
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AGENCOURT 14255831 NIH MGC 180 Homo sapiens cDNA clone
IMAGE:30386203 5', mRNA sequence.
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TTCTGTGACGGGTGTTGACAAAGAGATGATGCAAAGAATTAGAGAAAAATCTATTTTACA 300
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                                                   AGCAAATTAAAGAAGAAAAAAAAAAAAAAAAATAAAAATTAAGGGTCTTACTAGAAATTTGGCAT
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Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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High quality sequence start: 303
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Homo sapiens
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Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
CDNA Library Preparation: Miklos P. Brownstein (NHGRI), Shiraki
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM10769 row: p column: 18
High quality sequence stop: 671.
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602720472F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4837505 5',
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                                                                                                             362 GGAAATATTAAAATCAACTTCACCCTCGAGTATTCCCAACTGCACTCGTGAATCAAAA 421
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1. (bases 1 to 792)

NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
GTAGCAGAAGAGGAGGAGTGGCTACACAAACAAGCTGAGGCACGAAGAGAGCAATGAATACT
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/organism="Homo sapiens"
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/lab_host="DH108"
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                                         SILEGACIPOSEI SQUÍTYEL EMBYO LIBRARY LINEAR EST 29-JUL-2004 SILEGACIPOSEI SQUÍTYEL EMBYO LIBRARY I SPERMOPHÍLUS LATERALÍS CO738958
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Andrew R. Cossins
Laboratory for Environmental Gene Regulation
University of Liverpool
School of Biological Sciences, The Biosciences Building, Crown
Street, Liverpool, United Kingdom, L69 72B
Tel: +44(0)151-795-4431
Fax: +44(0)151-795-4431
Email: cossins@liv.ac.uk
Vector has been trimmed from this EST.
Plate: 21 row: p column: 08
Seq primer: pflc T7 (5'-AATACGACTCACTATAGGG-3')
High quality sequence stop: 793.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                              (bases 1 to 793)
Williams, D.R., Gracey, A.Y., Martin, S.L., Hughes, M.A., Li, W.,
Williams, D.R., Gracey, A.Y., Martin, S.L., Hughes, M.A., Li, W.,
Wigroarray analysis of transcriptional changes during hibernation
in the golden mantled ground squirrel, Spermophilus lateralis
Unpublished (2004)
                                                                                                                                                                                                                                 Spermophilus lateralis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 GAAGCAAAAGCTACAGCAAAGCGAGAAGATCAAAAATATACACTAAATGTCATGATGCAG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="embryo"
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/note="vector: pFLC; Site 1: Sal1 GTCGAG; Site 2: BamH1
GGATCC; Normalized and subtracted cDNA library prepared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACTAAAGCATTGGAAAGCCTGGAAAGAATATCAAAGAAAAAGCTGAGGAGCAAAAAAATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
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NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATC

cDNA Library Preparation: CLONTECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LinL at: image.llnl.gov
Plate: LLCM373 row: i column: 16

High quality sequence stop: 556.
                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 788)
                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGB:3685335"
                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                   GI:9808070
                                                 sapiens (human)
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pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (qrcgag); Oligo-dT primed using primer 5.-TTTTTTTTTTTTVN-3. size-selected for average insert size 2.2 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this
                                                                                                                                                                                                                                                   CTGCCCCTCAAAGGCGTGTGTGAGAGACACGGACGTGTTCTGCACGGAAAACTATCTG
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                                                                                                                                                                     Length 792;
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44.9%; Score 567.4; DB 4;
Best Local Similarity 91.5%; Pred. No. 5.5e-113;
Matches 671; Conservative 0; Mismatches 46;
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3' adaptor sequence: 3' adaptor sequence: 5' ATTCTAGAGGCGGACGACATG-dT(30)BN-3' (where B = A, C, C, or T) Average insert size 1.55 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."
/tissue_type="carcinoma, cell line"
/lab host="DH108 (T1 phage-resistant)"
/clonde="Organ: bladder; Vector: pDNR-LIB (Clontech);
Site 1: SflI (ggcgcctcggcc); Site 2: SflI
(ggcattatggcc); bobble-stranded cDNA was prepared from cell line RNA. 5, and 3' adaptors were used in cloning as fellows: 5' adaptor sequence: S'-CACGGCCATTATGGCC-3' and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 553; DB 2; Length 788;
Pred. No. 7.6e-110;
0; Mismatches 31; Indels
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94.6%;
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DEDOGASO 11 MAC_53 Homo sapiens CDNA clone IMAGE:3685335 5', mRNA sequence.

RESULT 6 BE564350 LOCUS DEFINITION

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Mus musculus adult male testis CDNA, RIKEN full-length enriched library, clone:1700010124 product:EKN1 homolog [Homo sapiens], full insert sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1019 TACACAAGGCTATTGAAGATTCTTCTAAGGCACTGGAATTATTGATGCCACCTGTTACAG 1078
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Sciurognathi, Muridae, Murinae, Mus
                                                                                     241 AGGAGTGGCTACACAAACAAGCAGGCACGAAGGGCAATGAATACTGAAATTCCTGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length to EMA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
                     TTACTGAGAAGTTAAAGGAAGACAGTATTCCTGCTCCTCGCTCTGTTGGCAGTATTAAAA
                                                                                                                                       TCAACTTTACCCCTCGAGTATTCCCAACAGCTCTTCGTGAATCACAAGTAGCAGAAGAGG
                                                                                                                                                                                                                                                                                                                                                    TGTTTGCAACGGAAAACTATTTGGCAGCTATCAATGCATATAATTTAGCCATAAGACTAA
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Mammalia; Eutheria; Rodentia;
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AKOO5832.1 GI:12838612
HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus
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Sus scrofa
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Susaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

1 (bases 1 to 683)
Susibili, H., Eguchi, T., Suzuki, K., Sawazaki, T., Toki, D., Shinkai, H., Okumura, M., Hamasima, N. and Awata, T.

PEDE (Pig EST Data Explorer): construction of a database for ESTs derived from pororine full-length cDNA libraries

L Nucleic Acids Res. 32 (1), D484-D488 (2004)
Contact: Hirohide Uenishi
Contact: Hirohide Uenishi
Contact: Hirohide Uenishi
Nucleic Agrobiological Sciences
2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan
Tel: +81-29-838-8627
Email: Huenishi@affrc.go.jp
Ext +81-29-838-8627
Email: huenishi@affrc.go.jp
EST project with full-length enriched cDNA libraries carried out in Animal Genome Research Program (Japan) by National Institute of Agrobiological Sciences and STARF-Institute
Single pass sequencing of clones derived from oligo-capped cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vector sequences were eliminated by RepeatMasker version 2002/07/13 and crossmatch version 0.990319
Low quality bases were trimmed based on the quality values.
                                                                                                                                                                                                                                                                                                                                                                                       BP460416 BP460416 tull-length enriched swine cDNA library, adult ovary Sus scrofa cDNA clone OVRM10147G01 5', mRNA sequence.
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Pred. No. 1.9e-102;
0; Mismatches 60;
                                                                                                                                                                                                                                                                   626
                                                                                                                                                                                                                                                                                   /dev_stage="adult"
/clone_lib="full-length
ovary"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="OVRM10147G01"
                                                                                                                                                                                                                                                                   TTACTAGAAATTTGGCATCTAGAAATCT
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BP460416.1 GI:40476478
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ilarity 90.2%;
Conservative 0
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Matches 555
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/db_xref="G1:26348135"
/translation="MSTDLPEFFDLKEBERNPDWLKDKGNKLFATENYLAAVDAYNLA
IRLNCKIPLLYLNRAACHLKLKOLHKAIEDSSKALELLTPPYADNANARMKAHVRRGT
AFCQLELYVEGLQDYEAALKIDPANTVVQNDAEKIRNIIQGTALKSRD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAGCCATAAGACTAAATAATAAGATGCCACTATTGTATTTGAACCGGGCTGCTTGCCACC 1003
                                                                                                                                                                                                                                                                                                                                                                                              118 TAAAACCTCGGGGTTTGCCCCGGAAGGCCCCACCACACCCCTCCCCACAAGAGGGAAGA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     764 AAGTAGCAGAAGAGGAGGAGTGGCTACACAAACAAGCTGAGGCACGAAGGCAATGAATA 823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGACATAGCTGAACTTTGCGATTTAAAAGAAGAAGAAAAAGAACCCAGAATGGTTGAAGG 883
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                                                                                                                                                                                                                                                                                                                                                                                                                                          704 TIGGCAGIATIAAAAICAACITIACCCCICGAGIATICCCAACAGCICTICGIGAAICAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   238 CTGGCAGTATTCAAATCAGCTTTACCCCTCGAGTGTTCCCAACAGCACTTCGGGAATCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    478 TAGCCATACGACTGAACTGTAAGATCCCATTATTGTATTTGAATCGGGCTGCTTGCCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1064 TGCCACCTGTTACAGACAATGCTAATGCAAGAATGAAGGCACATGTACGACGTGGAACAG
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                                                                                                                                                                                                                                                                                                    Score 513.8; DB 3;
Pred. No. 2.8e-101;
0; Mismatches 157;
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/note="putative"
1190
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Best Local Similarity 79.5%;
Matches 634; Conservative
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length CDNAs

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E (dases 1 to 1190)

Adachi, J., Alzawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakwa, T., Bono, H., Carninof, P., Fukuda, S., Fukunishi, Y., Ruruno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hort, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Komno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, Y., Iowa, C., Saito, H., Salto, R., Sakai, C., Sakai, K., Sano, H., Sagaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Takahashi, F., Tanaka, T., Tajami, M., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Yoshino, M., Muramatsu, M. and Hayashizaki, Y., Voshino, M., Muramatsu, M. and Hayashizaki, Y., Chima, Y., Chima, Y., Submission
. Jiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
Please visit our web site (http://genome.gsc.riken.jp/) for further
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'clone_lib="RIKEN full-length enriched mouse cDNA library"
                                                                                                                                                                                                                                                                               the RIKEN Genome Exploration Research Group Phase II Team and the
                                                                                                                                                                                                                                                                                                                                                                                            the FANTOM Consortium and the RIKEN Genome Exploration Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
                                                                                                                                                                                                                                                                                                                  Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
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/db_xref="taxon:10090"
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Musmalla; Butheria; Rodentia; Sciurognath; Muridae; Mutinae; Mammalla; Butheria; Rodentia; Sciurognath; Muridae; Mutinae; Musmanla; Butheria; Rodentia; Sciurognath; Muridae; Murinae; Musmanla; Butheria; Rodentia; Sciurognath; Muridae; Murinae; Mus. 1. Loses I to 917)

Nikaldo, I., Osato, M., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Mogami, A., Kiyosawa, H., Sagi, Y., Tomaru, Y., Hasegawa, Y., Mogami, A., Schonbach, C., Gojobori, T., Balda-elli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matuda, H., Batech, J., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Gustincich, S., Hirokawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kawaji, H., Kawasawa, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKensi, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Rawathadaran, S., Ravasa, Y., Lenhard, B., Loois, P., Schou, M., Schneider, C., Redi, J., Randchandran, S., Ravasa, Y., Taylor, M.S., Tasadah, R.D., Tasadah, R.D., Taskenka, Y., Taylor, M.S., Tasadah, R.D., Yanguina, J., Warardo, R., Wagner, L., Wanlestedt, C., Wang, Y., Waranbe, Y., Warando, R., Wagner, L., Wanlestedt, C., Wang, Y., Waranbe, Y., Hayatu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Saka, K., Sato, K., Kayawa, T., Kayawa, T., Kayawa, T., Kayawa, T., Waranishi, A., Hashizume, W., Lander, E.S., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogen, J., Bilmey, B. and Hayashizaki, Y. Rased on functional annotation of 60,770 full-length cDNAs
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Fre Institute of Physical and Chemical Research (RIKEN)
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Tel: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,
Ruda,S., Hashixume,W., Hayashida,K., Hirozane,T., Hori,F.,
Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y.,
Kondo,S., Konno,H., Koya,S., Miyazaki,A., Muraca,M., Nakamura,M.,
Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M.,
Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M., and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                            BY705981

BY705981 RIKEN full-length enriched, adult male testis Mus musculus cDNA clone 1700010124 5', mRNA sequence.
Contact: Yoshihide Hayashizaki
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_7558431 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6047052
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/lab_host="DHIOB (phage-resistant)"
/clone_lib="NIH MGC_72"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
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1 (bases 1 to 1131)
1MH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                         Context: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ArcC/DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information chtp://image.llnl.gov
http://image.llnl.gov
High quality sequence stop: 388.
Lication/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:6047052"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prepared by using trehalose thermo-activated reverse
transcriptuse and subsequently enriched for full-length by
cap-trapper. Second strand cDNA was prepared with the
primer adapter of sequence [5'
                                                                prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Sploration Research Group in Riken Genomic Science Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                585
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 CAGAGGAAGGAGAA---ACCGCTCGAGGAAAGCAAGCTGAAGG---ACCAAAGCTCTA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 AAACCTCGGGGTTTGCCCCGGAAGGCCCCACTCGCCTCCCCACACAAGAGGAAAT 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      236 GGCAGTATTCAAATCAGCTTTACCCCTCGAGTGTTCCCAACAGCACTTCGGGAATCCCAA 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTAGCAGAAGAGGAGGAGTGGCTACACAAACAAGCTGAGGCACGAAGAGCAATGAATACT 825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Computational Analysis of Full-Length Mouse cDNAs Compared with Numan Genome Sequences Mamm. Genome. 12, 673-677 (2001) Normalization and subtraction of cap-trapper-selected cDNAs to
                                                                                                                                                                                                                                                                                                                                              prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        466 ACTAAAGCATTGGAAGCCTGGAAAGAATATCAAAGAAAAGCTGAGGAGCAAAAAAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             586 AAATATAAGAGTCTTACTAGAAATTTGGCATCTAGAAATCTTGCTCCAAAAGGGAGAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCAGAAAATATTTACTGAGAAGTTAAAGGAAGACAGTATTCCTGCTCCTCGCTCTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            176 TGGGAAAACATATTTCCTGAGAAGTTAAAGGAAGACAGAGTCCCTGCGCCTCGCTCCGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 917;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tch
al Similarity 79.1%; Score 50%; DB 6; Length 91
al Similarity 79.1%; Pred. No. 4.9e-100;
630; Conservative 0; Mismatches 160; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             'organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'tissue_type="testis"
'dev_stage="adult"
'lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone="1700010124"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sex="male"
                                                                                                                                                                                                                                                                                                                                                                                             further details.
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Best Local Si
Matches 630;
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GCCATAAGACTAAATAATAAGATGCCACTATTGTATTTGAACCGGGCTGCTTGCCACCTA 1005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1126 TTCTGTCAACTAGAATTGTATGTAGAAGGCCTACAGGATTATGAAGCGGCCACTTAAGATT 1185
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601884034F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4102592 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1006 AAACTAAAAAACTTACACAAGGCTATTGAAGATTCTTCTAAGGCACTGGAATTATTGATG 1065
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/lab host."DH10B (T1 phage-resistant)"
/clone lib="NNH MGC 57"
/note="Organ: brain; Vector: pDNR-LIB (Clontech); Site_1:
Sfil (ggccgcctcggcc); Site_2: Sfil (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
                                                                                                                                                                                                                  416 AAGGGAAACAAATTGTTTGCAACAGAAACTATTTGGCAGCGGTTGATGCATATTTA 475
                                                                                                                                                                                                                                                                                                                                                                       476 GCCATACGACTGAACTGTAAGATCCCATTATTGTATTTGAATCGGGCTGCTTGCCACCTC 535
                                                                      356 GACCTTCCTGAGTTCTTTGACTTAAAAGAAGAGAGAGAATCCAGACTGGTTGAAAGAC 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            716 GACCCAGCCAACACAAGTGTACAGAACGATGCAGAGATTCCGATTATAATTCAAGGG 775
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Ammanla, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (Dases 1 to 545)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           536 AAATTAAAAAACCTACACAAGGCCATCGAGGACTCTTCTAAGGCACTAGAGTTATTGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                656 TTCTGTCAACTAAATTGTATGTTGAAGGCTTGCAAGATTATGAAACTGCACTTAAGATT
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:4102592"
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                                                                                                                                                                                                                                                                                                                                                                                          532
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                                                                                                                                                                                                                                                                                                     AAGCTGCAGCAAAGCGGGAAGATCAAAATACGCACTAAGTGTCATGATGAAGATTGAAG 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AATATATTTACTGAGAAGTTAAAGGAAGACAGTATTCCTGCTCCTCGCTCTGTTGGCAGT 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         712 ATTAAAATCAACTTTACCCCTCGAGTATTCCCAACAGCTCTTCGTGAATCACAAGTAGCA 771
                                  sequence: 5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30) BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.55 kb (range 0.9-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."
                                                                                                                                                                                                                                                                     09
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Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3'
                                                                                                                                                                                                                                                                                                                       GAATTAGAGAAAAATCTATTTTACAAGCACAAGAGAGAGCAAAAGAAGAAGCTACAGAAGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAGAGTCTTACTAGAAATTTGGCATCTAGAAATCTTGCTCCAAAAGGGAAAATTCAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7
                                                                                                                                                                     DB 2; Length 545;
                                                                                                                                                                                                     0; Mismatches 14; Indels
                                                                                                                                                                    38.7%; Score 488.6; DB 2
97.0%; Pred. No. 7.8e-96;
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McCray Lab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           University of Iowa
                                                                                                                                                                                                     Matches 519; Conservative
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DEFINITION
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KEYWORDS
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ORGANISM
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CN478982
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PUBMED
COMMENT
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TITLE
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2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
CDNA Library Dribaribution: Distribution information can be found at
thtp://genome.uiowa.edu/distribution/cf.html
The following repetitive elements were found in this CDNA
sequence: 133-243, > (GAAAA) #Simple repeat 493-514,
>AT rich#Low_complexity (matched compliment)
                                                                                                                                                                                                                                                                                                                                                                                                                       /moi type="mrRNA"
/db_xref="taxon:9606"
/clone="nur.C=rN0-afu-1-16-0-UI"
/tissue_type="Human Lung Epithelial cells"
/tissue_type="Human Lung Epithelial cells"
/tissue_type="Human Lung Forthologies) (T1 phage resistant)"
/clone lib="UJ-CF-FN0"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR 1; Site 2: Not 1;
UJ-CF-FN0 is a subtracted cDNA library derived from two normalized Human lung epithelial cell libraries (ENN and DU) The library was subtracted according to according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996; For additional information, contact:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           745
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTGAGGAGCAAAAAAATTCAGAGAGAGAAAATTATGTCAAAAAGAAAAGCAAATTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bento-soares@ulowa.edu
TAG TISSUE=Lung Epithelial Cells Tissue nos 359-368
TAG LIB=UT-CF-ENO
TAG_SEQ=GGCTGTAGGC"
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                                                                                                                                                                                                                                                                                                                                                                                                           organism="Homo sapiens"
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Matches 478;
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EST 28-FEB-2003
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 468)
Hellmann,I., Zollner,S., Enard,W., Ebersberger,I., Nickel,B. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Selection on human genes as revealed by comparisons to chimpanzee
                                                                              184 AAGAGCAAAGCCAAGATTGGAAATGACACGATTCTCTTCACATTGTATAAAAGGAGCCA
                                                                                                                                                                                                                                                                                                                           GAAAAATCTACTTGCAAGCACAGGAGAAAGCAAAAGGAGCTACAGAAGCGAAAGCTGCT
                                                                                                                                                                                                      244 GITCIGIGGAGAGCCITICIAIGECAGCGITGAAAAAAAAGAIGAIGAGAATAAAAA
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                                                                                                                                                     GCCATGTGGGGAGACCCTTTCTGTGACGGGTGTTGACAAAGAGATGATGAATTAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Paabo S
Evolutionary Genetics
Max. Planck-Institute for evolutionary Anthropology
Deutscher Platz 6, 04103 Leipzig, Germany
Flat: +49-(0)-341-3550 500
Fax: +49-(0)-341-3550 555
Email: paabo@eva.mpg.de
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Location/Qualifiers
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Pan troglodytes
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/mol_type="mRNA"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="InMAGE:7134374"
/tissue_type="testis, pooled"
/tissue_type="testis, pooled"
/tissue_type="testis, pooled"
/tissue_type="testis, pooled"
/clone lib="NIH MGC 238"
/clone lib="NIH MGC 238"
/clone lib="NIH MGC 238"
/clone lib="NIH MGC 238"
/clone lib="testis tissue of 8 wk old animal. Tissues were snap-frozen and kept at -80C before RNA extraction and purification (Tri-reagent method). cDNA was primed using oligo-dT primer:
5-pGACTAGTTCTAGATCGCGAGCGCCCC(C(7)25-3' and cloned into the ECORV/Not1 sites of pExpress-1. Size-selection >1.4kb resulted in an average insert size of 1.9 kb. This primary library is normalized (non-normalized primary library is NIH MGC 237) and was constructed by Express Genomics
                                                                                                                                                                                               CK603982 796 bp mRNA linear BST 22-JAN-2004 AGENCOURT 17890681 NIH MGC_238 Rattus norvegicus cDNA clone MAGE:7134374 5', mRNA sequence.
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Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics
National Cancer Institute / NIH

Bldg. 31 Rml0A07 Bethesda, MD 20892
Email: Gapbbs-remail.nin.gov
Tissue Procurement: Howard Jacobs

CDNA Library Preparation: Express Genomics

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC.Clone distribution information can be found through the I.M.A.G.E. Consortium/LLML at:

http://image.llnl.gov

Plate: LLAM15039 row: o column: 12

High quality sequence stop: 622.
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                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 796)
NIH+MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 449; DB 7;
Pred. No. 3.4e-87;
                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                           CK603982
CK603982.1 GI:41117319
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llarity 76.9%;
Conservative
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574; Conserv
866 ACCC 869
                                                          514 AGCC 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Si
Matches 574;
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VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                             DEFINITION
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TITLE
JOURNAL
COMMENT
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CK603982
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/organism="Homo sapiens"
/organism="Homo sapiens"
/mol type="mcNA"
/db xref="taxon:9606"
/clone="InMaS1:4081622"
/tlssue type="carcinoma, cell line"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NHH MGC_53"
/clone_lib="NHH MGC_53"
/clone_strainspecc; Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATATGGCC-3' and 3' adaptor sequence: 5'-CACGGCCATATGGC-3' and 3' adaptor sequence: 5'-CACGGCCATATGGCC-3' and 5' adaptor sequence: 5'-CACGGCCATATGGCC-
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLCM943 row: i column: 15
High quality sequence stop: 451.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCCATGTGGGAGACCCTTTCTGTGACGGGTGTTGACAAAGAAGATGATGCAAAGAATTAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  410 GCAAAGCGGGAAGATCAAAAATACGCACTAAGTGTCATGATGAACGATTGCAGAAGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAGGAAAAAAATAGAAGATATGA-----AAGAAAATGAACGGATAAAAGCCACTAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCCATGTGGGAGACCCTTTCTGTGACGGGTGTTGACAAAGAGATGATGCAAAGAATTAAGA
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Pred. No. 2.2e-82;
0; Mismatches 45; Indels 11
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89.8%;
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Best Local Similarity 89.8
Matches 495; Conservative
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                                                                     /tissue_type="brain, presumably cortex"
/dev_stage="adult"
/dev_stage="adult"
/dev_stage="bdict"
/dev_stage="bdict"
/clone_lib="Chimpanzee brain library Kcos"
/note="vector: pUChi; Site_1: Sfi1-A; Site_2: Sfi1-B; The library was prepared using the SMART cDNA library construction Kit (Clontech), doing only primer extension, but not PCR amplification of the cDNA. The only deviation from the published protocoll was that we cloned the cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGCCCCTCAAAGGCGTGTGCGTCAGAGACACGGACGTGTTCTGCACGAAAACTATCTG 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGCAGCAAAGCAAAAGATTGGGAATGACACCATTGTCTTCACCTTGTATAAAAAAGGAAGCG 269
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BF207765 1183 bp mRNA linear EST 06-NOV-20
601861861F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4081622 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATGCCTCTTCAGGTTAGCGATTACAGCTGGCAGACGAAGACTGCGGTCTTTCTGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 1183)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                              DB 6; Length 468;
                                                                                                                                                                                                                                                                                                                                                                         Score 434.2; DB 6; Length
Pred. No. 5.4e-84;
0; Mismatches 3; Indels
                         /clone="12B22058_rev_1_F09_r_075.abl"
/sex="male"
                                                                                                                                                                                                                                                                                                      into a plasmid Vector."
     xref="taxon:9598"
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ilarity 99.3%;
Conservative
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AUTHORS
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Search completed: July 8, 2005, 04:46:16 Job time : 4610 secs

us-10-681-199-1.rst

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Sequence 14, Appl
Sequence 1257, Ap
Sequence 1280, Ap
Sequence 16435, A
Sequence 5061, Ap
Sequence 5041, Ap
Sequence 6, Appl
Sequence 53, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1234, Ap
Sequence 30874, A
Sequence 34573, A
                                                                                                  8, 2005, 01:40:53; Search time 245 Seconds (without alignments) 8435.173 Million cell updates/sec
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Sequence 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/pcTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-621-976-1234
US-09-513-999C-30874
US-09-513-999C-31673
US-08-232-463-14
US-09-902-540-1357
US-09-902-540-1318
US-09-902-540-1318
US-09-902-540-1318
US-09-902-540-1318
US-09-270-767-5061
US-09-270-767-5031
US-09-270-767-5031
US-09-970-966-53
US-09-949-016-11760
US-09-949-016-11760
US-09-949-016-117323
US-09-949-016-117323
                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                        1202784 segs, 818138359 residues
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                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                    nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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1263
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Match Length
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No.
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Sequence 193, App Sequence 191, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 13770, A Sequence 1531, A Sequence 1531, A Sequence 1662, A Sequence 1668, A Sequence 14373, A Sequence 1331, A Sequence 1331, A Sequence 1335, A Sequence 1335, A Sequence 3, Appli		Length 489; Indels 0; Gaps 0; AGACTGCGGTCTTTCTGTCT 60 AGACTGCGGTCTTTCTGTCT 116 AGACTGCGGAAAACTATCTG 120 TCTGCACGGAAAACTATCTG 176 ATGCTCCCATAGACGATGAG 180 ATGCTCCCATAGACGATGAG 236 CCTTGTATAAAAAAGCGG 296 AGATGATGCAAAGAATTAGA 300 GAATGATGCAAAGAATTAGA 356 CTACAGAAAGCAAAAGCTGCA 360 CTACAGAAAGCAAAAGCTGCA 360 CTACAGAAAGCTAGCA 316
3 US-09-461-697-193 3 US-09-461-697-191 3 US-09-461-697-189 3 US-09-461-697-187 3 US-09-461-697-187 3 US-09-461-697-187 4 US-09-916-13770 1 US-08-257-073-4 5 US-09-171-209-8 4 US-09-949-016-15821 5 US-09-949-016-15821 5 US-09-949-016-15831 6 US-09-949-016-15831 7 US-09-949-016-15831 8 US-09-949-016-1688 8 US-09-949-016-1688 9 US-09-949-016-1688 9 US-09-949-016-1688 9 US-09-949-016-1688	ALIGNMENTS IS/09621976 Irds, J.B. id Encoded Human Proteins R2 US/09/621,976 07-21	34.3%; Score 432.6; DB 4; Length 489; imilarity 99.8%; Pred. No. 4.6e-97; Conservative 1; Mismatches 0; Indels 0; Gaps Argccrcrrcaggrragggarracagggaggaggaggaggaggaggaggaggaggaggagga
66.2 5.2 699 66.2 5.2 774 66.2 5.2 774 66.2 5.2 1165 66.2 5.2 1165 66.2 5.1 223 66.4 5.1 223 64.6 5.0 588 63.6 5.0 588 63.6 5.0 588 63.4 5.0 12703 63.4 5.0 12703 62.4 4.9 54033 62.4 4.9 54033	RESULT 1 US-09-621-976-1234 Sequence 1234, Application US/09621976 Patent No. 6639063 Replicant: Dumas Milne Edwards, J.B. APPLICANT: Dumas Milne Edwards, J.B. APPLICANT: Glordano, J.Y. TIPLE OF INVENTION: ESTG and Encoded Human Profits Reference: Genser. 054PR2 CURRENT APPLICATION UNDERS: US/09/621,976 CURRENT FILING DATE: 2000-07-21 NUMBER OF SEQ ID NOS: 19335 SEQ ID NO 1234 LENGTH: 489 TYPE: DAA OGGANISM: Homo sapiens FEATURE: NAME/KEY: CDS UGCATION: 57.488 US-09-621-976-1234	Ouery Match Best Local Similarity 99.8%; Matches 432, Conservative 1 ArGCTCTTCAGGTTAGG 57 ATGCTCTTCAGGTTAGG 117 CTGCCCTCAAAGGCGTC 121 AAGGTCAACTTTCTCCCC 121 AAGGTCAACTTTCTCCCC 121 AAGGTCAACTTTCTCCCC 122 AAGGTCAAAGCAAAGATT 181 AGCACCAAAGCAAAGATT 182 AGCACCAAAGCAAAGATT 182 AGCACCAAAGCAAAGATT 183 AGCACCAAAGCAAAGATT 184 AGCACCAAAGCAAAGATT 185 AGCACCAAAGCAAAGATT 186 AGCACAAAACCATTTACAA 187 AGCAAAAATCTATTTACAA 188 AGAAAAATCTATTTACAA 189 AGAAAAATCTATTTACAA
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 1 US-09-621-976 ; Sequence 12 ; Patent No. ; FAPLICANT: ; APPLICANT: ; APPLICANT: ; APPLICANT: ; TITLE OF II ; TITLE OF I	Query Matches Matches Oy

Sequence 14, Appl Sequence 13234, A Sequence 184917,

2447 25431 601 601 194937

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Sequence 185072, Sequence 17032, A Sequence 17033, A

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Indels
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Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: SCHETFLINGER, F.
APPLICANT: SCHETFLINGER, F.
APPLICANT: PALKNER, F.
APPLICANT: SCHETFLINGER, F.
APPLICANT: FOLEVER F.
STREET: 1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12.9%; Score 162.8; DB 4; 98.8%; Pred. No. 9.9e-31; tive 2; Mismatches 0;
                                                                            1021 CACAAGGCTATTGAAGATTCTTCTAAGGCACT 1052
                                                                                              181 CACAAGGCTATTGAAGATTCTTCTAAGGAATT 212
                                                                                                                                                                                                              Sequence 34573, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: h=a or c or t US-09-513-999C-34573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: 127
OTHER INFORMATION: y=c or t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 98.8'
Matches 162; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature LOCATION: 128
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STATE: VA
COUNTRY: USA
                                                                                                                                                                                              JS-09-513-999C-34573
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US-513-999C-30874

Sequence 30874, Application US/09513999C

Sequence 30874, Application US/09513999C

Sequence 30874, Application US/09513999C

APPLICANT: Duclert, A.

APPLICANT: Duclert, A.

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

PALENT G. SERENCE: 59.US2.REG

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

PALLOR PELICANT: 000-02-24

CURRENT APPLICATION NUMBER: US/09/513,999C

CURRENT FILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681

SOFTWARE: PATENT.

LENGTH: 313

LENGTH: 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                904 GCAACGGAAAACTATTTGGCAGCTA--TCAATGCATAT-AATTTAGCCATAAGACTAAAT 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    417 GCAAAGCGGGAAGATCAAAAATACGCACTAAGTGTCATGATGATGATGAAGAAGAAGAAGAG 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GATTTAAAAGAAGAAGAAGAAGACCAGAATGGTTGAAGGATAAAGGAAACAAATTGTTT 60
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Pred. No. 1.5e-34;
5; Mismatches 3; Indels
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US-09-513-999C-30874
                                                                                                                                      477 AGGAAAAAAAA 489
                                                                                                  421 AGGAAAAAATAG 433
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Best Local Similarity 94.8
Matches 201; Conservative
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LOCATION: 250
OTHER INFORMATION: n=a,
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LOCATION: 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
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NAME/KEY: misc_feature
LOCATION: 82
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65 CCCTCAAAGGCGTGTGCGTCAGAGACACGGACGTGTTCTGCACGGAAAACTATCTGAAGG 124
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                                                                                                                                                                                                                                                                                                             APPLICANT: Duclert, A. A. APPLICANT: Duclert, A. A. APPLICANT: Duclert, A. A. APPLICANT: Duclert, A. A. APPLICANT: Giordano, Jr.Y. TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins. Patent No. 678361
FILE REPERBORE: 59.022.REG CURRENT APPLICATION NUMBER: US/09/513,999C CURRENT APPLICATION NUMBER: US/09/513,999C PRIOR PAPLICATION NUMBER: US 60/122,487
PRIOR PLING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SSC ID NO 34573
LENGTH: 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CTCTTCAGGTTAGCGATTACAGCTGGCAGCAGACGAAGACTGCGGTCTTTCTGTCTCTGC
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ORGANISM: Myxococcus xanthus
                 Barry S.
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                                                                                                                                                                                                                                                FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 358 GCAGCAAAGCGGGAAGATCAAAAATACGCACTAAGTGTCATGATGAAGATTGAAGAAA 417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        598 CTTACTAGAAATTTGGCATCTAGAAATCTTGCTCCAAAAGGGAGAAATTCAGAAAATATA 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           658 TTTACTGAGAAGTTAAAGGAAGACAGTATTCCTGCTCCTCGCTCTGTTGGCAGTATTAAA 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 7.0%; Pred. No. 1.7e-18;
Matches 30; Conservative 271; Mismatches 128; Indels
                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                           APPLICATION NUMBER: EP 91 114 300.6 FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INPORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.2%; Score 115.8;
                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                          FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                      TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                         TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTAATTCT 1023
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                                                                                                                                                                   FILING DATE:
                                                                                                      FILING DATE
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; Sequence 1357, Application US/09902540

-09-902-540-1357

RESULT 5 US-09-902

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455 GGATAAAAGCCACTAAAGCATTGGAAGCCTGGAAAGAATATCAAAGAAAAGCTGAGGAGC 514
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
CURRENT PAPLICATION NUMBER: US/09/902,540
CURRENT PILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 1357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Stare, Steven C.
APPLICANT: Stare, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REPERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: 60/9902,540
CURRENT FILING DATE: 2001-07-10
PRIOR PILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 1280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 275 ACAAAGAGATGATGCAAAGAATTAGAGAAAATCTATTTTACAAGCACAAGAGAGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            515 AAAAAAATTCAGAGAGAAGAGAAATTATGTCAAAAAGAAAAGCAAATTAAAGAAGGAA
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Best Local Similarity 51.2%; Pred. No. 9.5e-13;
Matches 209; Conservative 0; Mismatches 199; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: unsure
LOCATION: (1)..(612)
OTHER INFORMATION: unsure at all n locations
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US-09-949-016-16435; Sequence 16435; Sequence 16435; Patent No. 6812339; GENERAL INFORMATION:
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Best Local Similarity 51.7<sup>†</sup>
Matches 167; Conservative
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US-09-949-016-16435
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Sequence 1318, Application US/09902540

Patent No. 6833447

GENERAL INFORMATION:

APPLICANT: Goldman, Barry S.

APPLICANT: Alater, Steven C.

APPLICANT: Wiegand, Roger C.

TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof

FILE REFERENCE: 38-10(1549)B

CURRENT PILING DATE: 2001-07-10

PRIOR PILING DATE: 2001-07-10

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825

SEQ ID NO 1318
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                                                                                                                        Score 77.4; DB 4; Length 1039;
Pred. No. 2.4e-09;
0; Mismatches 182; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION: (1)..(614)
; OTHER INFORMATION: unsure at all n locations
US-09-902-540-1318
                                                           ; NAME/KEY: unsure
; LOCATION: (1)..(1039)
; OTHER INFORMATION: unsure at all n locations
US-09-902-540-1280
                                                                                                                        Query Match 6.1%;
Best Local Similarity 50.5%;
Matches 186; Conservative
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                    TYPE: DNA ORGANISM: Myxococcus xanthus
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GENERAL INCOMENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PAPLICATION NUMBER: 60/237,768
PRIOR PLING DATE: 2000-10-20
PRIOR PLING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-06
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                  AAAAAAAATTCAGAGAAGAAGAAATTATGTCAAAAAGAAAAGCAAATTAAAGAAGGAA 574
335 AAGAAGCTACAGAAGCAAAAGCTGCAGCAAAGCGGGAAGATCAAAAATACGCACTAAGTG 394
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Pred. No. 2.1e-07;
0; Mismatches 156;
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Query Match
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TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILLE REFERENCE: FILE REFERENCE: FILE REFERENCE: Tale Reference: 7226-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT PILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5661
LENGTH: 705
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TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REPERENCE: FILE REFERENCE: FILE REPERENCE: FILE REPERENCE: TOWNERN. US/09/270,767
CURRENT APPLICATION NUMBER: US/09/270,767
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 20343
LENGTH: 705
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51.8%; Pred. No. 3.1e-08;
tive 0; Mismatches 194; Indels
                              122787 AAGAAAGAAAGAAAGAAAGAAAG 122809
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                                                                                                                    Sequence 5061, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-5061
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US-09-270-767-20343
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 51.8<sup>†</sup>
Matches 216; Conservative
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US-09-270-767-5061
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324 AGAGAGAGCAAAAGAAGCTACAGAAGCAAAAGCTGCAGCAAAGCGGGAAGATCAAAAATA 383
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                                                  Gaps
                                                7;
5.7%; Score 72.6; DB 4; Length 7
51.8%; Pred. No. 3.1e-08;
7ative 0; Mismatches 194; Indels
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Patent No. 5627054

GENERAL INFORMATION:
TITLE OF INVENTION: COMPETITOR PRIMER ASYMMETRIC
TITLE OF INVENTION: POLYMERASE CHAIN REACTION
NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:
ADDRESSEE: U.S. ARMY CHEMICAL AND BIOLOGICAL
ADDRESSEE: DEFENSE COMMAND
STREET: OFFICE OF THE CHIEF COUNSEL (AMSCB-GC)
CITY: ABERDEEN PROVING GROUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC_compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/628,417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BIFFONI, ULYSSES J
REGISTRATION NUMBER: 39,908
REFERENCE/DOCKET NUMBER: DAM 398-94
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 21010-5423
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 410-671-1158
TELEFAX: 410-671-2534
                         Best Local Similaricy ....
Matches 216; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
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SEQ ID NO 53
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                                                                                                                                                                                         430 ATAGAAGATATGAAAGAAAATGAACGGATAAAAGCCACTAAAGCATTGGAAGCCTGGAAA 489
                                                                                                                                                                                                                    190 GAATATCAAAGAAAAGCTGAGGAGCAAAAAAAAATTCAGAGAGAAGAGAAATTATGTCAA 549
                                                                                                                                                                                                                                                                             11 ĠĄCĄĄTĄŻĄŻĄCTŢTĄĠŻĄTŢĄĄTŢTŢĄCTĄŻĄĄĄŻĄŻĄŻĄŻĄŻĄŻĄŻĄŻĄŻĄŻĄŻĄŻĄŻĄŻĄŻ
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                                                                                                                                                                                                                                                                                                          Score 72; DB 4; Length 396;
Pred. No. 3.4e-08;
0; Mismatches 111; Indels
                                                                                                   96; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 53, Application US/09640173

Patent No. 6613515

GENERAL INPORMATION:
APPLICANT: Xu, Janagchun
APPLICANT: Xu, Janagchun
TITLE OF INVENTION: OVARIAN TUMOR SEQUENCES AND
TITLE OF INVENTION: METHODS OF USE THEREFOR
FILE REFERENCE: 210121.484C2
CURRENT APPLICATION NOMBER: US/09/640,173
CURRENT APPLICATION NOMBER: US/09/640,173
CURRENT APPLICATION NOMBER: 2000-08-15
NUMBER OF SEQ ID NOS: 196
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 53
LENGTH: 396
                                                                    Score 72.4; DB 1;
Pred. No. 2.2e-08;
                                                                                                   0; Mismatches
oligodeoxynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY: misc feature
; LOCATION: (1)...(396)
; OTHER INFORMATION: n = A,T,C or G
US-09-640-173-53
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                                                                    Query Match
Best Local Similarity 57.5%;
Matches 130; Conservative
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Best Local Similarity 54.9
Matches 135; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapien
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MOLECULE TYPE:
            HYPOTHETICAL:

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US-08-628-417-6
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US-09-640-173-53/c
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363 AAAGCGGGAAGATCAAAAATACGCACTAAGTGTCATGATGAAGATTGAAGAAGAAGAGAG 422
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| Sequence 53, Application US/09825294 |
| Patent No. 6710170 |
| GENERAL INFORMATION: |
| APPLICANT: XU Jiangchun |
| APPLICANT: Algate, Paul A. |
| TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER |
| TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER |
| TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER |
| TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER |
| TITLE OF INVENTION: 2010.04-03 |
| CURRENT FILING DATE: 2001.04-03 |
| SOFTWARE PEASESE FOR WINDOWS Version 3.0 |
| SEQ ID NO 53 |
| LENGTH: 396 |
         Sequence 53, Application US/09713550
; Patent No. 6617109
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Xt, Jiangchun
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
; FILE REPERENCE: 210121.484C4
; CURRENT APPLICATION NUMBER: US/09/713,550
; CURRENT PILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 205
; SOFTWARE: FASTERQ for Windows Version 3.0
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Best Local Similarity 54.9%; Pred. No. 3.4e-08;
Matches 135; Conservative 0; Mismatches 111; Indels
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NAME/KEY: misc feature

LOCATION: (1)...(396)

OTHER INFORMATION: n = A,T,C or G
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ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
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ORGANISM: Homo sapien
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LOCATION: 224, 225, 228, 235, 240, 246, 257, 266, 274, 279, 281, LOCATION: 283, 286, 287, 288, 290, 291, 292, 293, 294, 295, 296, LOCATION: 300, 301, 303, 307, 311, 313, 314, 317, 318, 319, 320, 310, 301, 302, 311, 313, 314, 317, 318, 319, 320, THER INFORMATION: n = A,T,C or G
NAME/KEY: misc_feature
LOCATION: 342, 343, 344, 345, 346, 347, 348, 349, 350, 351, 352, LOCATION: 357, 358, 359, 362, 363, 364, 365, 367, 373, 380, OTHER INFORMATION: n = A,T,C or G
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Batent No. 6720146

GENERAL INFORMATION:
APPLICANT: Stolk, John A.
APPLICANT: Fling, Steven P.
APPLICANT: Fling, Steven P.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER FILE REPRENCE: 210121.484C6
CURRENT APPLICATION NUMBER: US/09/970,966
CURRENT FLING DATE: 2001-10-02
NUMBER OF SEQ ID NOS: 215
SOFTWARE: FASELSEQ for Windows Version 4.0
IENGTH: 396
                                                                         Query Match 5.7%; Score 72; DB 4; Length 396; Best Local Similarity 54.9%; Pred. No. 3.4e-08; Matches 135; Conservative 0; Mismatches 111; Indels
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; LOCATION: (1)...(396)
; OTHER INFORMATION: n = A,T,C or G
US-09-825-294-53
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ORGANISM: Homo sapiens
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US-09-970-966-53/c
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1: /cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
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Maximum Match 100%
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10 US-10-10-85-30001
10 US-09-918-995-22675
10 US-09-918-995-10303
11 US-10-956-157-314
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21 US-10-312-841-2
21 US-10-313-957-3
22 US-10-313-957-3
23 US-10-313-957-3
24 US-10-425-115-38710
25 US-10-425-115-38710
26 US-10-425-115-38710
27 US-10-313-955-109
28 US-10-425-115-387-3888
29 US-10-311-455-1692
20 US-10-311-455-1692
21 US-10-363-345A-23588
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ALIGNMENTS

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1 ATGCCTCTTCAGGTTAGCGATTACAGCTGGCAGCAGACGAAGACTGCGGTCTTTCTGTCT
Sequence 1, Application US/10364505
Publication No. US20030219787A1
GENERAL INFORMATION:
APPLICANT: Taipale, Mikko
APPLICANT: Rere, Jule
APPLICANT: Raminen, Nina
APPLICANT: Raminen, Nina
TITLE OF INVENTION: NOVEL HUMAN GENE FUNCTIONALLY RELATED TO DYSLEXIA
FILE REPERROE: 0933-0199P
CURRENT APPLICATION UNDHER: US/10/364,505
CURRENT FILING DATE: 2003-02-12
NUMBER OF SEQ ID NOS: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: coding sequence for human DYXC1 (cDNA)
US-10-364-505-1
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Result Š.

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; NAME/KEY: CDS
; LOCATION: (369)..(1628)
; FEATURE:
; OTHER INFORMATION: human DYXC1 mRNA as cDNA
US-10-364-505-2
                                                   Query Match
Best Local Similarity 100.
Matches 1263; Conservative
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Publication No. US20030219787A1
GENERAL INFORMATION:
APPLICANT: Kere, Juha
APPLICANT: Taipale, Mikko
APPLICANT: Kaninen, Niaa
APPLICANT: No. US20030219787A10la-Hemmi, Jaana
APPLICANT: No. US20030219787A10la-Hemmi, Jaana
APPLICANT: No. US20030219787A10la-Hemmi, Jaana
APPLICANT: No. US20030219787A10la-Hemmi, Jaana
APPLICANT: NOVEL HUMAN GENE FUNCTIONALLY RELI
FILE REFERENCE: 0933-0199P
CURRENT APPLICATION UNMER: US/10/364,505
CURRENT APPLICATION UNMER: US/10/364,505
CURRENT FILING DATE: 2003-02-12
NUMBER OF SEQ ID NOS: 13
SEQ ID NO 2
LENGTH: 1993
TYPE: DNA
CREANISM: Homo sapiens
FEATURE:
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1029 ACTGAGAAGTTAAAGGAAGACAGTATTCCTGCTCCTCGCTCTGTTGGCAGTATTAAAATC 1088 1208 TGCGATTTAAAAGAAGAAGAAAAGAACCCAGAATGGTTGAAGGATAAAGGAAACAAATTG 1268 900 960 GAAAAATCTATTTTACAAGCACAAGAGAGAGAGCAAAAGAAGCTACAGAAGCAAAAGCAGCA crececercaaaeecererecercaaeacaeeecerererecaeeaaaaerarere AAGGTCAACTITCCTCCAFTTTTATTTGAGGCATTTCTTTATGCCCCCATAGACGATGAG **AGGAAAAAAATAGAAGATATGAAAGAAAATGAACGGATAAAAGCCACTAAAGCATTGGAA** AGGAAAAAAATAGAAAGTATGAAAGAAAATGAAAGGATAAAAAGCCACTAAAAGCATTGGAA 969 ACTAGAAATTTGGCATCTAGAAATCTTGCTCCAAAAGGGAGAAATTTCAGAAAATATATT Argecterricagerragegarracagergecageagacgagacracagererrerer CTGCCCCTCAAAGGCGTGTGCGTCAGAGACACGGACGTGTTCTGCACGGAAAACTATCTG AAGGTCAACTTTCCTCCATTTTTATTTGAGGCATTTCTTTATGCTCCCATAGACGATGAG GCCATGTGGGAGACCCTTTCTGTGACGGGTGTTGACAAAGAGAGATGATGCAAAGAATTAGA GAAAAATCTATTTTACAAGCACAAGAGAGAGCAAAAGAAGCTACAGAAGCAAAAGCTGCA ACTAGAAATTTGGCATCTAGAAATCTTGCTCCAAAAGGGAGAAATTCAGAAAATATTTT 1149 GACTGGCTACACAAACAGAGGCACGAAGAGGCAATGAATACTGACATAGCTGAACTT GCCATGTGGGAGACCCTTTCTGTGACGGGTGTTGACAAAGAGATGATGCAAAGAATTAGA ACTGAGAAGTTAAAGGAAGACAGTATTCCTGCTCCTCGCTCTGTTGGCAGTATTAAAATC AACTTTACCCCTCGAGTATTCCCCAACAGCTCTTCGTGAATCACAAGTAGCAGAAGAGGAG TITGCAACGGAAAACTATITGGCAGCTATCAATGCATATATTTAGCCATAAGACTAAAT GAGTGGCTACACAAACAAGCTGAGGCACGAAGAGCAATGAATACTGACATAGCTGAACTT TGCGATTTAAAAGAAGAAGAAAGAACCCAGAATGGTTGAAGGATAAAGGAAACAAATTG Gaps ö Length 1993; ATGCCTCTTCAGGTTAGCGATTACAGCTGGCAGCAGACGAAGACTGCGG Indels 100.0%; Score 1263; DB 17; 100.0%; Pred. No. 5.9e-253; iive 0; Mismatches 0;

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US-10-681-199-19
Sequence 19, Application US/10681199
; Publication No. US20040138441A1
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                     CTGCCCCTCAAAGGCGTGTGCGTCAGAGACACGGCGTGTTCTGCACGGAAAACTATCTG
                                                                                         AATGCTAATGCAAGAATGAAGGCACATGTACGACGTGGAACAGCATTCTGTCAACTAGAA
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                                                                                                                                                                                                                                                                                 Sequence 2, Application US/10681199
; Publication No. US20040138441A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL HUMAN GENE FUNCTIONALLY RELATED TO DYSLEXIA
TITLE OF INVENTION: NOVEL HUMAN GENE FUNCTIONALLY RELATED TO DYSLEXIA
TITLE OF INVENTION: NOVEL HUMAN GENE FUNCTIONALLY RELATED TO DYSLEXIA
CURRENT PAPLICATION WHOBER: US/10/681,199
CURRENT FILING DATE: 2003-10-09
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 2
LENGTH: 1993
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Best Local Similarity 100.0%; Pred. No. 5.9e-253;
Matches 1263; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: human DYXC1 mRNA as CDNA
US-10-681-199-2
                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
LOCATION: (369)..(1628)
                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                 TAA 1263
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US-10-681-199-2
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TITLE OF INVENTION: NOVEL HUMAN GENE FUNCTIONALLY RELATED TO DYSLEXIA
FILE REPERENCE: 0933-0214P
CURRENT APPLICATION NUMBER: US/10/681,199
CURRENT FILING DATE: 2003-10-09
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 13
LENGTH: 1263
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Pred. No. 1.1e-250;
0; Mismatches 7; Indels
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; LOCATION: (1)..(1260)
US-10-681-199-13
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           APPLICANT: KERE, Juha
TITLE OF INVENTION: NOVEL HUMAN GENE FUNCTIONALLY RELATED TO DYSLEXIA
FILE REPRENCE: 0933-0214P
CURRENT APPLICATION NUMBER: US/10/681,199
CURRENT FILING DATE: 2003-10-09
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 19
LENGTH: 1263
                                                                                                                                                                                                                                                                        DB 19; Length 1263
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Pred. No. 5e-251;
0; Mismatches 6; Indels
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Best Local Similarity 99.5%;
Matches 1257; Conservative
                                                                                                                                                         TYPE: DNA
ORGANISM: Pan paniscus
                                                                                                                                                                                                    ) NAME/KEY: CDS
; LOCATION: (1)..(1260)
US-10-681-199-19
GENERAL INFORMATION:
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                                                                                                          APPLICANT: KERE, Juha
TITLE OF INVENTION: NOVEL HUMAN GENE FUNCTIONALLY RELATED TO DYSLEXIA
TITLE REFERENCE: 0930-02149
CURRENT APPLICATION NUMBER: US/10/681,199
CURRENT FILING DATE: 2003-10-09
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
                                                                                                                                                                                                                                                                                           Length 1263
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Pred. No. 5e-250;
0; Mismatches 9; Indels
                                                 RESULT 7
US-10-681-199-15
'Sequence 15. Application US/10681199
'Publication No. US20040138441A1
'GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 99.3%;
Matches 1254; Conservative
                                                                                                                                                                                                                TYPE: DNA ORGANISM: Gorilla gorilla
                                                                                                                                                                                                                                                       , LOCATION: (1)..(1260)
US-10-681-199-15
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Best Local Similarity
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NAME/KEY: CDS
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                       AGCAGCAAAGCAAAAGATTGGGAATGACACCATTGTCTTCTCACCTTGTATAAAAAAGAAGCG
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Best Local Similarity 99.0%; Pred. No. 5e-249;
Matches 1251; Conservative 0; Mismatches 12; Indels
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; LOCATION: (1)..(1260)
US-10-681-199-17
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; Sequence 4, Application US/10364505
; Publication No. US20030219787A1
; GENERAL INFORMATION:
    APPLICANT: Kere, Juha
    APPLICANT: Taipale, Mikko
; APPLICANT: Kaminen, Nina
; TITLE OF INVENTION: NOVEL HUMAN GENE FUNCTIONALLY RELATED TO DYSL
; FILE REFERENCE: 0933-0199P
; CURRENT APPLICATION NUMBER: US/10/364,505
; UNRENT FILING DATE: 2003-02-12
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NOS: 13
; SEQ ID NO 4
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ORGANISM: Mus musculus
FEATURE:
NAME/KEY: CDS
LOCATION: (48)..(1307)
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Pred. No. 4.3e-208;
0; Mismatches 1; Indels 0; (
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Publication No. US20040005560A1

GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/10/108,260A

CURRENT APPLICATION NUMBER: US/10/108,260A

NUMBER OF SEQ ID NOS: 5458

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 575

LENGTH: 1559
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 1048; Conserv
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                                                                                                                         Sequence 4, Application US/10681199
PUblication No. US20040138441A1
GENERAL INFORMATION:
APPLICANT: KERE, Juha
FILTE OF INVENTION: NOVEL HUMAN GENE FUNCTIONALLY RELATED
CURRENT APPLICATION NUMBER: US/10/681,199
CURRENT APPLICATION NUMBER: 2003-10-09
NUMBER OF SEQ 1D NOS: 42
SOFTWARE: Patentin Ver. 2.1
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Pred. No. 4.7e-165;
0; Mismatches 242;
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Sequence 30001, Application US/10085783A

Sequence 30001, Application US/10085783A

Publication No. US20040037841A1

GENERAL INFORMATION:
APPLICANT: Chondrogene Inc.
TILE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REPRENCE: 4231/2002

TILLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REPRENCE: 4231/2002

CURRENT FILING DATE: 2002-02-28

PRIOR FILING DATE: 2001-07-13

PRIOR FILING DATE: 2001-03-12

PRIOR FILING DATE: 2001-03-12

PRIOR FILING DATE: 2001-03-12

PRIOR FILING DATE: 2001-03-28

NUMBER OF SEQ ID NOS: 58994

SOFTWARE: PatentIn version 3.2

LENGTH: 464
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                                                                                                                                                                                                                                     Length 464;
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; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (321)...(321)
; OTHER INFORMATION: n is a, c,;
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (347)...(347)
; OTHER INFORMATION: n is a, c,
US-10-242-535A-30001
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NAME/KEY: misc_feature
LOCATION: (263)..(263)
OTHER_INFORMATION: n is a,
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Best Local Similarity 98.3
Matches 404; Conservative
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NAME/KEY: misc feature
LOCATION: (321)..(321)
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Sequence 30001, Application No. US20040013663A1

GENERAL INFORMATION:
APPLICANT: ChondroGene Inc.
APPLICANT: ChondroGene Inc.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2005
CURRENT FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US/10/242,535A
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR PILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR PILING DATE: 2001-03-12
PRIOR PILING DATE: 2001-03-12
PRIOR PILING DATE: 2001-03-12
PRIOR FILING DATE: 2001-03-12
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SPRIOR FILING DATE: 2001-03-12
PRIOR FILING DATE: 2001-03-12
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  GAGTGGCTGCATAAACAAGCAGAAGCACGGAGAGCCATGAGCACTGACCTTCCTGAGTTC 881
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NAME/KEY: misc feature
LOCATION: (263). (263)
OTHER INFORMATION: n is a, c, g, or t
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ORGANISM: Human
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Pred. No. 4e-60;
0; Mismatches 35; Indels
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Publication No. US20030073623A1
GENERAL INFORMATION:
APPLICATION:
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROW VARIOUS CDNA LIBRARIES
TILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT APPLICATION NUMBER: US/09/235,076
PRIOR APPLICATION NUMBER: US/09/235,076
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SOFTWARE: FastSEQ for Windows Version 3.0,
SEQ ID NO 10303
LENGTH: 458
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| LOCATION: (1)...(458)
| THEN INFORMATION: n = A,T,C or G
| US-09-918-995-10303
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Best Local Similarity 91.1:
Matches 368; Conservative
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US-09-918-995-10303
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                                                                                                                  Query Match 31.8%; Score 401.6; DB 18; Length 464; Best Local Similarity 98.3%; Pred. No. 8.7e-74; Matches 404; Conservative 0; Mismatches 7; Indels 0;
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; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: HYSEQ, Inc.
; TITLE OF INVENTION: ROWEL NUCLBIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: ROW VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT PILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR PILING DATE: 1999-01-20
; NUMBER OF SEC ID NOS: 38054
; SOFTWARE: FastSEQ for Windows Version 3.0
; TENERM. 600
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Pred. No. 3.7e-67;
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Best Local Similarity 99.5%;
Matches 371; Conservative
             FRATURE:
NAME/KEY: misc feature
LOCATION: (347)...(347)
COTHER INFORMATION: n is a,
OTHER INFORMATION: n is a,
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; ORGANISM: Homo sapiens
US-09-918-995-22675
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US-09-918-995-22675
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Sequence 872, App Sequence 10303, A Sequence 1114, Ap Sequence 30901, A Sequence 30001, A Sequence 7, Appli Sequence 7, Appli Sequence 8, Appli Sequence 8, Appli

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Sequence 1, Application US/10364505;
Publication No. US20030219787A1
GENERAL INFORMATION:
APPLICANT: Taipale, Mikko
APPLICANT: No. US20030219787A10la-Hemmi, Jaana
APPLICANT: No. US20030219787A10la-Hemmi, Jaana
APPLICANT: No. US20030219787A10la-Hemmi, Jaana
TITLE OF INVENTION: NOVEL HUMAN GENE FUNCTIONALLY RELATED TO DYSLEXIA
FILE REFERENCE: 0933-0199P
CURRENT APPLICATION NUMBER: US/10/364,505
CURRENT FILING DATE: 2003-02-12
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 1263
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US-10-364-505-1
9 US-10-681-199-15

9 US-10-681-199-17

0 US-10-240-425-872

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1 US-10-956-157-8144

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Copyright (c) 1993 - 2005 Compugen Ltd.
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Score

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OY 1141 TTGTATGTAGAAGGCCTACAGGATTATGAAGCGGCACTTAAGATTGATCCATCC	O%; Score 1263; DB 19; O%; Pred. No. 0; O; Mismatches O;	OY 1 AIGCTCTTCAGGTTAACAGCTGGGAGCAACAACAACTGCGGTCTTTCTGTCT 60 1 AIGCCTCTTCAGGTTAACAGTTACAGCTGGCAACAACAACAACAGACTGCGGGTCTTTCTGTCT 60	Qy 61 CTGCCCTCAAAGGCGTGTGCGTCAGAGACACGGACGTGTTCTGCACGGAAACTATCTG 120 Db CTGCCCTCAAAGGCGTGTGCGTCAGAGACACGGACGTGTTCTGCACGGAAAACTATCTG 120	Qy 121 AAGGICAACTITCCTCCAITITATITIGAGGCAITICITIAIGCTCCCAIAGACGAIGAG 180	Oy 181 AGCAGCAAAGATTGGGAATGACACATTGTCTTCACCTTGTATAAAAAGGAGG 240	Qy 241 GCCATGTGGGAGACCCTTTCTGTGACGGGTGTTGACAAAGAGATGATGCAAAGAATTAGA 300 11	Qy 301 GAAAAATCTATTTACAAGAGAGAGAGAGAAAAGAAGAGAGAAGCAAAAGCTGCA 360 	OY 361 GCAAAGCGGGAAGATCAAAAATACGCACTAAGTGTCATGATGAAGATTGAAGAAGAAGAG 420 11	Oy 421 AGGAAAAAATAGAAGATATGAAAGAAAATGAAGGATAAAAGCCCCTAAAGCATTGGAA 480	Qy 481 GCCTGGAAAGAATATCAAAGAAAAGCTGAGGAGCAAAAAAATTCAGAGAGAAAAA 540 Db 481 GCCTGGAAAGAATATCAAAGAAAAAGTGGGAGCAAAAAAATTCAGAGAGAAAAA 540
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US-10-364-505-2
| Sequence 2, Application US/10364505
| Publication No. US20030219787A1
| GENERAL INFORMATION:
| APPLICANT: Raipale, Mikko
| APPLICANT: Raipale, Mikko
| APPLICANT: Raipale, Mikko
| APPLICANT: Raminen, Nina
| TILLE REFERENCE: 0933-0199P
| CURRENT FILING DATE: 2033-0199P
| CURRENT FILING DATE: 2033-02-12
| NUMBER OF SEQ ID NOS: 13
| SOFTWARE: PatentIn Ver. 2.1
| SEQ ID NO 2
| LENGTH: 1993
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ORGANISM: Homo sapiens
PEATURE:
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                                                                                                            100.0%; Score 1263;
100.0%; Pred. No. 0;
ive 0; Mismatches
; NAME/KEY: CDS
; LOCATION: (369)..(1628)
; PEATURE:
; OTHER INFORMATION: human DYXC1 mRNA as CDNA
US-10-364-505-2
                                                                                                          Query Match 100.
Best Local Similarity 100.
Matches 1263; Conservative
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1329 AATAAGATGCCACTATTGTATTTGAACCGGGCTGCTTGCCACCTAAAAACTAAAAACTTA 1388
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US-10-681-199-19
Sequence 19, Application US/10681199
Publication No. US20040138441A1
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; Publication No. US20040138441A1
; Publication No. US20040138441A1
; Publication No. US20040138441A1
; APPLICANT: KERE, Juha
; TITLE OF INVENTION: NOVEL HUMAN GENE FUNCTIONALLY RELATED TO DYSLEXIA
; FILE REFERENCE: 0933-0214P
; CURRENT APPLICATION WHEER: US/10/681,199
; CURRENT PELING DATE: 2003-10-09
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIN Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1993
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100.0%; Pred. No. 0;
ive 0; Mismatches
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US-10-681-199-2
                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 1263; Conservative
                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Homo sapiens FEATURE: NAME/KEY: CDS LOCATION: (369)..(1628)
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US-10-681-199-2
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Pred. No. 0;
0; Mismatches 5; Indels 0;
       APPLICANT: KERE, Juha
TITLE OF INVENTION: NOVEL HUMAN GENE FUNCTIONALLY RELATED TO I
FILE REPRENEUR: 0933-0014P
CURRENT APPLICATION NUMBER: US/10/681,199
CURRENT FILING DATE: 2003-10-09
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 19
LENGTH: 1263
                                                                                                                                                                           Query Match
Best Local Similarity 99.6%;
Matches 1252; Conservative
                                                                                                   TYPE: DNA
ORGANISM: Pan paniscus
                                                                                                                        ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1260)
US-10-681-199-19
GENERAL INFORMATION:
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; Publication No. US20040005560A1
; GENERAL INPORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA
; PILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: Patentin Ver. 2.1
; SRQ ID NO 575
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 1048; Conservative 0; Mismatches 1;
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CORGANISM: Homo sapiens
US-10-108-260A-575
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                          Score 960; DB pred. No. 0; O; Mismatches
                          76.0%;
illarity 99.6%;
Conservative 0
; LOCATION: (1)..(1260)
US-10-681-199-13
                          Query Match
Best Local Similarity
Matches 1210; Conser
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 GCCATGTGGGGAGACCCTTTCTGTGACGGGTGTTGACAAAGAGATGATGCAAAGAATTAGA 342
                               AACTTTACCCCTCGAGTATTCCCAACAGCTCTTCGTGAATCACAAGTAGCAGAAGAGAGGAG
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                     GAAAAATCTATTTACAAGCACAAGAGAGAGAAAAGAAGCTACAGAAGCAAAAGCTGCA
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TITLE OF INVENTION: NOVEL HUMAN GENE FUNCTIO
FILE REFERENCE: 0933-0214P
CURRENT APPLICATION NUMBER: US/10/681,199
CURRENT FILIME DATE: 2003-10-09
CURRENT FILIME DATE: 201
SOFTWARE: PatentIn Ver. 2.1
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
TYPE: DNA
TYPE: DNA
CORGANISM: Pan troglodytes
FRATURE:
NAME/KEY: CDS
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Publication No. US20040138441A1
GENERAL INFORMATION:
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                                                         CAGTATTAAAATCAACTTTACCCCTCGAGTATTCCCAACAGCTCTTCGTGAATCACAAGT
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                     TAAAGAATTGGAAGCCTGGAAAGAATATCAAAGAAAAGCTGAGGAGCAAAAAGAAATTCA
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Publication No. US20040138441A1
GENERAL INFORMATION:
APPLICANT: KERE, JUHA
TITLE OF INVERTION: NOVEL HUMAN GENE FUNCTIONALLY RELATED TO DYSLEXIA
TITLE OF INVERTION: NOVEL HUMAN GENE FUNCTIONALLY RELATED TO DYSLEXIA
FILE REFERENCE: 0933-0214P
CURRENT APPLICATION UNMBER: US/10/681,199
CURRENT FILING DATE: 2003-10-09
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 17
IENGTH: 1263
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ORGANISM: Pongo pygmaeus
FEATURE:
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US-10-681-199-17
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CTAAAAAACTTACACAAGGCTATTGAAGATTCTTCTAAGGCACTGGAATTATTGATGCCA
                                                            CCTGTTACAGACAATGCAAGAATGAAGGCACATGTACGACGTGGAACAGCATTC
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Sequence 15, Application US/10681199
Publication No. US20040138441A1
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE REFERENCE: 0933-02149
CURRENT APPLICATION NUMBER: US/10/681,199
CURRENT PILING DATE: 2003-10-09
NUMBER: OF SEQ ID NOS: 42
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
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68.0%; Score 859; DB 19; Length 1263;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1209; Conservative 0; Mismatches 7; Indels 0
                                                                                                                                                                                                                                                                 1249 GAACTAAAATCTTAA 1263
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; LOCATION: (1)
US-10-681-199-15
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                                       GCTATTGAAGATTCTTCTAAGGCACTGGAATTATTGATGCCACCTGTTACAGACAATGCT
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; Sequence 22675. Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
    APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: REOM VARIOUS CDNA LIBRARIES
    TITLE OF INVENTION: REOM VARIOUS CDNA LIBRARIES
; TITLE OF INVENTION: REOM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT PILING DATE: 2001-07-30
pRIOR APPLICATION NUMBER: US/09/235,076
; WUMBER OF SEQ ID NOS: 38054
; SEQ ID NOS: 38054
; SEQ ID NO 22675
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Best Local Similarity 100.0%; Pred. No. 1.7e-151;
Matches 326; Conservative 0; Mismatches 0;
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US-10-240-425-872/c
; Sequence 872, Application US/10240425
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                                                       DB 19;
                                                     Score 696; DB
Pred. No. 0;
0; Mismatches
                                                       55.1%;
99.1%;
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                  ..(1260)
                                                     Query Match
Best Local Similarity
Matches 1246; Conserv
     ; NAME/KEY: CDS
; LOCATION: (1)
US-10-681-199-17
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US-10-240-425-872
                               APPLICANT: Williams, Amanda
APPLICANT: Boland, Joseph F.
APPLICANT: Lord, Reginald V.
APPLICANT: Alvarez, Chris
APPLICANT: Werzel, Jon C.
APPLICANT: Scherf, Uwe
APPLICANT: Scherf, Uwe
APPLICANT: Vockley, Joseph G.
APPLICANT: Vockley, Joseph G.
APPLICANT: Vockley, Gone Expression Profiles in Esophageal Tissue
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; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: PAPEL OF INVENTION:
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: PROM VARIOUS CDNA LIBRARIES
; FILER REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995.
; PRIOR PILING DATE: 2001-07-30
; PRIOR PILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTHARE: PRAESEQ for Windows Version 3.0
; SEQ ID NO 10303
LENGTH: 458
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100.0%; Pred. No. 5.2e-151;
tive 0; Mismatches 0; Indels
                                                                                                                                                                      FILE REFERENCE: 44921-5026
CURRENT APPLICATION NUMBER: US/10/240,425
CURRENT FILING DATE: 2002-09-30
PRIOR APPLICATION NUMBER: PCT/US01/09847
PRIOR FILING DATE: 2001-03-28
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 1588
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 872
LENGTH: 325
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Publication No. US20040033502A1
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Matches 325; Conservative
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ORGANISM: Homo sapiens
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US-09-918-995-10303
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APPLICANT: Wyeth APPLICANT: Wyeth APPLICANT: Wyeth APPLICANT: Wyeth APPLICANT: Wounts, William APPLICANT: Wounts, William TITLE OF INVENTION: WOCKEC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES FILE REFERENCE: 031896-043000 (AM 101081) CURRENT APPLICATION NUMBER: US/10/956,157 CURRENT APPLICATION NUMBER: US/10/956,157 NUMBER OF SEQ ID NOS: 319805 SOFTWARE: Patentin version 3.2 SEQ ID NO 3114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           953 GACTAAATAATAAGATGCCACTATTGTATTTGAACCGGGCTGCTTGCCACCTAAAACTAA 1012
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                                                                                                                                                                                          21.4%; Score 270; DB 10; Length 4 100.0%; Pred. No. 1.4e-123; tive 0; Mismatches 0; Indels
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100.0%; Pred. No. 4.2e-115;
iive 0; Mismatches 0;
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Publication No. US20050118625A1
GENERAL INFORMATION:
                                                                    | NAME/KEY: misc_feature
| LOCATION: (1)...(458)
| OTHER INFORMATION: n = A,T,C or G
US-09-918-995-10303
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Best Local Similarity 100.(
Matches 253; Conservative
                                                                                                                                                                                                                                               Matches 270; Conservative
TYPE: DNA ORGANISM: Homo sapiens
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US-10-956-157-3114
                                                                                                                                                                                          Query Match
Best Local Similarity
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49 ATGCCTCTTCAGGTTAGCGATTACAGCTGGCAGCAGACGAGAGACTGCGGTCTTTCTGTCT 108
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| NAME/KEY: misc feature
| LOCATION: (347) ... (347)
| OTHER INFORMATION: n is a, c, g, or t
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                                                                                                                                        Sequence 8349, Application US/10956157
| Publication No. US20050118625A1
| GENERAL INFORMATION:
| APPLICANT: Wyeth
| APPLICANT: Wounts, William | APPLICANT: Wounds: US/10/956,157 | CURRENT PILING DATE: 2004-10-04 | NUMBER OF SEQ ID NOS: 319805 | SOFTWARE: Patentin version 3.2 | SEQ ID NO 8349 | LENGTH: 715
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KEBOUL 12

KEBOUL 142-535A-30001

KENERAL 10001, Application US/10242535A

Publication No. US20040013663A1

GENERAL INFORMATION:

APPLICANT: ChondroGene Inc.

APPLICANT: Liew, C.C.

TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis

FILE REFERENCE: 4231/2005

CURRENT APPLICATION NUMBER: US/10/242,535A

CURRENT FILING DATE: 2002-09-12

PRIOR APPLICATION NUMBER: US 60/305,783

PRIOR PILING DATE: 2001-03-12

PRIOR PILING DATE: 2001-03-12

PRIOR APPLICATION NUMBER: US 60/275,017

PRIOR PILING DATE: 2001-03-12

PRIOR PILING DATE: 2001-03-12

PRIOR PILING DATE: 2001-03-28

NUMBER OF SEQ ID NOS: 58994

SOFTWARE: PatentIn version 3.2

LENGTH: 464
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/clone lib="NIH MGC_179"
/note="Organ: brain; Vector: pCMV-SPORT6.1; Site_1: ECORV (destroyed); Site_2: Not1; Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.1 kb. Library was constructed by (Invitrogen). Note: this is a NIH_MGC
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NIH-MGC http://mgc.nci.nih.gov/.

L Onpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein

CDNA Library Preparation: Invitrogen Corp

CONA Library Preparation: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/Link at:

Found through the I.M.A.G.E. Consortium/Link at:

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                                                                            Length 1600;
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Pred. No. 0;
0; Mismatches
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       /note="Vector: pDNR-LIB"
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University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CLORD Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/cf.html
The following repetitive elements were found in this CDNA
sequence: 133-243, >(GAAAA)n#Simple repeat 493-514,
>AT_rich#Low_complexity (matched compliment)
Seq primer: M13 FORWARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CN478982 53-APR-2004
UI-CF-FN0-afu-l-16-0-UI.81 UI-CF-FN0 Homo sapiens CDNA clone
UI-CF-FN0-afu-l-16-0-UI 3', mRNA sequence.
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Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                      AAGACAGTATTCCTGCTCCTCGCTCTTTTGTTTAAAATCAACTTTACCCCTCGAG
AGCACAAGAGAGGAAAAGAAGCTACAGAAGCAAAAGCTGCAGCAAAGCGGGAAGATCA
                                                       421 TATGAAAGAAAATGAACGGATAAAAGCCACTAAAGCATTGGAAGCCTGGAAAGAATATCA
                                                                                                     438 TATGAAAGAAAATGAACGGATAAAAGCCACTAAAAGCATTGGAAGCCTGGAAAGAATATCA
                                                                                                                                                                         AAGAAAAGCTGAGGAGCAAAAAAAAATTCAGAGAAGAAGAAATTATGTCAAAAAGAAA
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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Homo sapiens
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TITLE
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CN478982
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/tissue_type="Human Lung Epithelial cells"
/tissue_type="Human Lung Epithelial cells"
/lab host="DH10B (Life Technologies) (TI phage resistant)"
/clome_lib="UI-CF-FN0"
/clome_lib="UI-CF-FN0"
/note="Togan: Lung; Vector: pT713-Pac (Pharmacia) with a modified polylinker; Site_l: EcoR 1; Site_2: Not 1;
UI-CF-FN0 is a subtracted_cDNA library derived from two normalized Human lung epithelial cell libraries (EN1 and DU1) The library was subtracted according to according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. For additional information, contact:
bento-soares@ulowa.edu
TAG_IISSUE=Lung Epithelial Cells Tissue nos 359-368
TAG_LIB-UI-CF-FN0
TAG_LIB-UI-CF-FN0
TAG_SEQ_GGCTGTAGGC"
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AGENCOURT 7558431 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6047052
5', mRNA sequence.
BQ217312
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11 HMG http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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36.6%; Score 462; DB 7; Le
Best Local Similarity 100.0%; Pred. No. 5.4e-225;
Matches 462; Conservative 0; Mismatches 0;
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Tissue Procurement: ATCC/DCTD/DTP
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788 bp mRNA linear EST 15-AUG-2000 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685335 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="GRN_PREHEP"
/note="oligo dT_primed, full-length enriched cDNA library
from DMSO-treated hES cell line H9 (p22) maintained in
feeder-free conditions"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATGCCTCTTCAGGTTAGCGATTACAGCTGGCAGCAGACGAAGACGCGGCTGCTGTTCTGTTT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          161 AAGSTCAACTTTCCTCCATTTTTATTTGAGGCATTTCTTTATGCTCCCATAGACGATGAG 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 GAAAAATCTATTTTACAAGCACAAAGAGGAAAAAGAAGCTACAGAAGCAAAAGCTGCA 360
Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
Lebkowski,J and Stanton,L.W.
Transcriptome characterization elucidates signaling networks that
control human Es cell growth and differentiation
Nat. Blotechnol. 22 (6), 707-716 (2004)
                                                                                                                                                                                                                                                                                                                                 cells, DMSO-treated H9 cell
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0
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                                                                                                           Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
TH: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 462 Std Error: 0.00.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33.4%; Score 422; DB 7; Le
100.0%; Pred. No. 1.7e-204;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:9606"
/tiseue_type="embryonic stem
line"
                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             601343161F1 NIH_MGC_53
mRNA sequence.
BE564350
BE564350.1 GI:9808070
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BE564350
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17000600026401 GRN_PREHEP Homo sapiens cDNA 5', mRNA seguence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone lib="NIH MGC_72"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGCTCCCATAGACGATGAGAGCAGCAAAGCAAAGATTGGGAATGACACCATTGTCTTCAC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTTGTATAAAAAGAAGCGGCCATGTGGGAGACCCTTTCTGTGACGGGTGTTGACAAAGA 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTTGTATAAAAAGAAGCGGCCATGTGGGAGACCCTTTCTGTGACGGGTGTTGACAAAGA 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42 GACTGCGGTCTTTCTGTCTCTGCCCCTCAAAGGCGTGTGCGTCAGAGACACGGACGTGTT 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGCACGGAAAACTATCTGAAGGTCAACTTTCCTCCATTTTTATTTGAGGCATTTCTTTA 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGCTCCCATAGACGATGAGAGCAGCAAGGAAAGATTGGGAAATGACACCATTGTCTTCAC 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TACAGAAGCAAAAGCTGCAGCAAAGCGGGAAGATCAAAAATACGCACTAAGTGTCATGAT 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 TACAGAAGCAAAAGCTGCAACAAAGCGGGAAGATCAAAAATACGCACTAAGTGTCATGAT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAAGATTGAAGAAGAAGAGAGAAAAAAAATAGAAGATATGAAAGAAAATGAACGGATAAA 461
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 462)
Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GATGATGCAAAGAATTAGAGAAAAATCTATTTTACAAGCACAAGAGAGCCAAAAAGAAGC
                                                               þe
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     cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can l
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13293 row
High quality sequence stop: 388.
High quality sequence stop: 388.
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                                                                                                                                                                                                                                                                                                                                                                                                                        35.3%; Score 446; DB 5; Length 1131;
100.0%; Pred. No. 9.1e-217;
tive 0; Mismatches 0; Indels (
                                                                                                                                                                                         /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6047052"
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CN429788.1 GI:47417382
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Best Local S:
Matches 446
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VERSION
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Gaps

9

120

180

240

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/organism="Homo sapiens"

/mol_type="mRNA"

/db_txefe="txxxxn:960"

/db_txefe="txxxn:960"

/clone="type="carcinoma, cell line"

/lab host="but10B (T1 phage-resistant)"

/clone lib="NTH MGC 53"

/clone lib="NTH MGC 53"

/note="Organ: bladder; Vector: pDNR-LIB (Clontech);

/note="Organ: bladder; Vector: pDNR-LIB (Clontech);

/site_l: Sfil (ggccgcctcggcc); Site_2: Sfil

/ggccattarggcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCCATTATGGCC-3' and 3' adaptor sequence: 5'-CACGCCCATTATGGCC-3' and 3' adaptor sequence: 5'-CACGCCCATTATGGCC-3' and 3' adaptor sequence: 5'-CACGCCCATTATGGCC-3' and 5' adaptor sequence: 5'-CACGCCATTATGGCC-3' and 5' adaptor sequence: 5'-CACGCCATTATGGCC-3' and 5' adaptor sequence: 5'-CACGCCATTATGGCC-3' and 5' adaptor sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAAAAATCTATTTTACAAGCACAAGAGAGCAAAAGAAGCTACAGAAGCAAAAGCTGCA 360
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 788)
                                                                                                                                                                                                                      Contact: Rober Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCS

CDNA Library Preparation: CLONTECH Laboratories, Inc.

CDNA Library Preparation: CLONTECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: LLCM373 row: i column: 16

High quality sequence stop: 556.
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                                                                                                   1 .03583 1.0 /08)
MIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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/mol_type="mRNA"
/mol_type="mRNA"
/db xref="taxon:9606"
/clone=lib="NHAGE:6614647"
/lab host="DHIOB (TI phage-resistant)"
/clone=lib="NHH MGC 82"
/clo
AGENCOURT 10398893 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:6614647 BU567908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180
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                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbe.remail.nih.gov
Tissue Procurement: CLONTECH
CDNA Library Preparation: CLONTECH
Laboratories, Inc.
CDNA Library Preparation: CLONTECH
Laboratorium (LiNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCN2855 row: h column: 07
High quality sequence stop: 540.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 823)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
                                                                                                                                                                                 BU567908.1 GI:22918208
                                                                                                                                                                                                                                                           Homo sapiens (human)
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SOURCE
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CD358543 913 bp mRNA linear EST 29-MAY-2003
AGENCOURT 14255831 NIH MGC_180 Homo sapiens CDNA clone
IMAGE:30386203 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361 GCAAAGCGGGAAGATCAAAAATACGCACTAAGTGTCATGATGAAGATGAAGAAGAAGAG 420
241 GCCATGTGGGAGACCCTTTCTGTGACGGGTGTTGACAAAGAGATGATGCAAAGAATTAGA 300
                                                                                           301 GAAAAATCTATTTACAAGCACAAGAGAGAGCAAAAGAAGCTACAGAAGCAAAAGCTGCA 360
                                                                                                                                                                                                            397 GCAAAGCGGGAAGATCAAAAATACGCACTAAGTGTCATGATGAAGATTGAAGAAGAAGAG 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-WGC http://mgc.nci.nih.gov/.

NIH-WGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-remail.nih.gov

Tissue Procurement: Dr. Michael Brownstein

cDNA Library Preparation: Invitrogen Corp

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: NDAM454 row: h column: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 933)
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/lab_host="DH10B-Ton A ( T1 and T5 phage resistances)"
/clone_lib="NIH_MGC_180"
                           Gaps
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llarity 99.8%; Pred. No. 7.3e-180;
Conservative 0; Mismatches 1;
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/organism="Homo sapiens"
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High quality sequence stop: 666.
Location/Qualifiers
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/db_xref="taxon:9606"
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Shift-MGC thtp://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1959)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
CDNA Library Preparation: Michael J. Brownstein (LIML)
DNA Sequencing by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at:
http://image.llnl.gov
Plate: LiAMIOT69 row: p column: 18
High quality sequence stop; 671.
High quality sequence stop; 671.

Location/Qualifiers
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                                                                                                                                                                  BG771796 792 bp mRNA linear EST 15-MAY-2001 602720472F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4837505 5',
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 792)
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Pred. No. 6.4e-182;
0; Mismatches 1; Indels
    361 GCAAAGCGGGAAGATCAAAATACGCACTAAGTGTCATGATGAAG 405
                           412 GCAAAGCGGGAAGATCAAAAATACGCACTAAGTGTCATGATGAAG 456
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/db_xref="taxon:9606"
/clone="IMAGE:4837505"
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Best Local Similarity 99.8%;
Matches 428; Conservative
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Producement: James Martin
Tissue Producement: James Martin
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@ulowa.edu
The following repetitive elements were found in this cDNA
sequence: 1-44, AT rich#Low_complexity (matched compliment)
POLYAA'SE.
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UI-H-FLO-bdk-g-13-0-UI.sl NCI CGAP_FLO Homo sapiens cDNA clone
UI-H-FLO-bdk-g-13-0-UI 3', mRNA sequence.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 772)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
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                                                       28.8%; Score 364; DB 2; Le
100.0%; Pred. No. 9.4e-175;
ive 0; Mismatches 0;
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/db_xref="texaon:9606"
/clone="UI-H-FLO-bdk-g-13-0-UI"
/tissue_type="Cell lines"

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    organism="Homo sapiens"

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Alto, CA)."
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BE972748.1 GI:10586084
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                  AAGACAGTATTCCTGCTCCTCGCTCTGTTGGCAGTATTAAAATCAACTTTACCCCTCGAG 736
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1 (bases 1 to 573)

NIH-MGC http://mgc.nci.nih.gov/.

National institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
                                                                                              CTAGAAATCTTGCTCCCAAAAGGGAGAAATTCAGAAAATATATTTACTGAGAAGTTAAAGG
                                                                                                                                                                                                                                                           553 AAGACAGTATTCCTGCTCCTCGCTCTGTTGGCTATTAAATCAACTTTACCCCTCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found 'through the I.M.A.G.E. Consortium/LINL at:
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High quality sequence stop: 571.
Location/Qualifiers
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/lab host="DH10B (Life Technologies)"
/clone lib="NCI CGAP FLO"
/note="Organ: Chondrosarcoma; Vector: pT773-Pac
/hote="Organ: Chondrosarcoma; Vector: pT773-Pac
(Pharmacia) with a modified polylinker; Site_1: EcoR I;
Site_2: Not I; NCI CGAP FLO is a cDNA library derived from a pool of mRNA obtained from 4 cell lines from grade III
chondrosarcoma tissues. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GAGGTCGGTG. The cell line was provided by Dr James Martin from University of Iowa.

TAG_IISSIE=Human Chondrosarcoma Grade 3 cell line mix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1041
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 468)
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12B22058 rev 1 F09 r_075.abl Chimpanzee brain library Koos Pan
troglodytes cDNA clone 12B22058_rev_1_F09_r_075.abl 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    982 TIGAACCGGGCTGCTTGCCACCTAAAAACTTAAAAACTTACAAAGGCTATTGAAGATTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        660 TIGAACCGGCCTGCTTGCCACCTAAAACTAAAAACTTACACAAGGCTATTGAAGATTCT
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Evolutionary Genetics
Max-Planck-Institute for evolutionary Anthropology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       27.1%; Score 342; DB 6; Le
100.0%; Pred. No. 1.8e-163;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                            TAG SEQ=GAGGTCGGTG"
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Matches 342, Conservative
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/tissue_type="brain, presumably cortex"
/dev stage="adult"
/lab_host="Epicurian Coli (TM) XL-10-Gold"
/clone_lib="Chimpanzee brain library Koos"
/note="vector: pUChi; Site 1: Sfil-A; Site 2: Sfil-B; The library was prepared using the SMART cDNA library construction Kit (Clontech), doing only primer extension, but not PCR amplification of the cDNA. The only deviation from the published protocoll was that we cloned the cDNA into a plasmid Vector."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        349 GCAAAAGCTGCAGCAAAAAGCGGGAAGATCAAAAATACGCACTAAGTGTCATGATGAAATT 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAAAAAGAAGCGGCCATGTGGGAAGACCCTTTCTGTGACGGGTGTTGACAAAGAGATGATG 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            258 AAAAAAGAAGCGGCCATGTGGGAAGCCCTTTCTGTGACGGGTGTTGACAAAGAGATGATG 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 417)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GICTITCTGTCTCTGCCCTCAAAGGCGTGTGCGTCAGAGACACGGACGTCTGCACG
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                                                                                                                                                                                                                                  /clone="12B22058_rev_1_F09_r_075.ab1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26.9%; Score 340; DB 6; L 99.7%; Pred. No. 1.9e-162; ive 0; Mismatches 1;
04103 Leipzig, Germany
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/mol_type="mRNA"
/db_xref="taxon:9598"
                                                                                                                  Location/Qualifiers
                   Tel: +49-(0)-341-3550 500
Fax: +49-(0)-341-3550 555
Email: paabo@eva.mpg.de
Seq primer: M13 reverse.
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                                                                                                                                                                                                                                                                /sex="male"
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Matches 390; Conserv
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sapiens (human)
                                                                                                                                        Tumor Gene Index
Unpublished (1997)
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                     Homo sapiens
Homo sapiens
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Best Local Simi
Matches 325;
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 KEYWORDS
SOURCE
ORGANISM
                                                                                                       AUTHORS
TITLE
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                                                                                     REFERENCE
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                                                                                                                                                                                                                                                                                                                         /clone lib="Soares testis NHT"
/note="Vector: pT7T3D-Pac"(Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Ecore. Library and Eco RI sites of the modified pT713 vector. Library went through one round of normalization to CO5, and was constructed by Bento Soares and M. Patima Bonaldo.
                                                                                                       Sequencing Center information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AI783611 325 bp mRNA linear EST 16-DEC-1999 tz99c0l.x1 NCI CGAP Kidl1 Homo sapiens cDNA clone IMAGE:2296704 3' similar to contains Alu repetitive element;, mRNA sequence. AI783611. GI:5325420
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                                                     M. Fatima
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0
                              Email: cgapbe-remail.nih.gov
CDNA Library Preparation: M. Bento Soares, Ph.D., M.
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequ
Clone distribution: NCI-CGAP clone distribution info
found through the I.M.A.G.B. Consortium/Link at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40ml3 fwd. ET from Amersham.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 26.8%; Score 338; DB 1; Length 417; Best Local Similarity 99.7%; Pred. No. 2e-161; Matches 388; Conservative 0; Mismatches 1; Indels
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                 Ph.D.
                                                                                                                                                                                                                            /organism="Homo sapiens"
                                                                                                                                                                                                                                                                            clone="IMAGE:1643738"
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 Unpublished (1997)
Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                            /sex="male"
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                                                                                                                                                                                                        1. .417
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 437 Std Error: 0.00

Seq primer: -40UP from Gibco
High quality sequence stop: 325.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab.host="DH108"
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/clone lib="NCI CGAP Kidl1"
/note="Organ: kidney; Vector: pT713D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not 1; Site 2: Eco R1;
Plasmid DNA from the normalized library NCI CGAP Kid3 was
prepared, and se circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneIDs 132276-1323911, 1456007-1456775, and
1500552-1502855). Subtraction by Bento Soares and M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                763
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  764 AAGTAGCAGAAGAGGAGGAGTGGCTACACAAACAAGCTGAGGCACGAAGAGGCAATGAATA 823
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 355)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          325 TTCAGAGAGAAGAAATTATGTCAAAAAGAAAAGCAAATTAAAGAAGAAGAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                265 TAAAATATAAGAGTCTTACTAGAAATTTGGCATCTAGAAATCTTGCTCCAAAAGGGGAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            584 TAAAATATAAGAGTCTTACTAGAAATTTGGCATCTAGAAAATCTTGCTCCAAAAGGGAGAA
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Pred. No. 8.9e-155;
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100.0%; Pred. No. co...
0; Mismatches
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/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                               AGENCOURT 10501009 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:6619012 5', mRNA sequence.
BU852580
BU852580.1 GI:24037543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 CTCGCCACCTAAAAACTAAAAACTTACACAAGGCTATTGAAGATTCTTCTAAGGCACTGG 182
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                                                                                                                                                                                                                                 Homo sapiens (human)
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Best Local S:
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Oy 1235 TAATTCAAGGAACA 1248
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Db 363 TAATTCAAGGAACA 376
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Search completed: July 8, 2005, 12:03:37 Job time : 9626 secs